Sinedden
10/007363
Seq. ID 2

GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: March 14, 2003, 09:17:19 ; Search time 36 Seconds
(without alignments)
29.611 Million cell updates/sec

Title: US-10-007-363-2
Perfect score: 48
Sequence: 1 HDAPIGYD 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*
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2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	48	100.0	8	19	AAW54884	Isozyme-specific a
2	43	89.6	8	19	AAW54889	Isozyme-specific a
3	43	89.6	8	19	AAW54892	Isozyme-specific a
4	42	87.5	8	19	AAW54894	Isozyme-specific a
5	42	87.5	8	19	AAW54895	Isozyme-specific a
6	42	87.5	11	18	AAW17460	Protein kinase C-e
7	40	83.3	8	19	AAW54887	Isozyme-specific a
8	40	83.3	8	19	AAW54888	Isozyme-specific a
9	40	83.3	8	19	AAW54890	Isozyme-specific a
10	40	83.3	8	19	AAW54891	Isozyme-specific a
11	39	81.2	8	19	AAW54893	Isozyme-specific a
12	38	79.2	8	19	AAW54898	Isozyme-specific a
13	37.5	78.1	14	19	AAW54901	Isozyme-specific a
14	35	72.9	6	19	AAW54886	Isozyme-specific a
15	35	72.9	8	19	AAW54885	Isozyme-specific a
16	35	72.9	14	22	AAG73329	Protease indicator
17	35	72.9	287	21	AAB43941	Human cancer assoc
18	35	72.9	456	17	AAR94933	Mouse immunophilin
19	35	72.9	456	23	ABB57096	Mouse ischaemic co
20	35	72.9	457	17	AAR94934	Human immunophilin
21	35	72.9	649	23	ABP39046	Staphylococcus epi
22	35	72.9	793	22	ABG25597	Novel human diagno
23	35	72.9	1247	22	ABG24986	Novel human diagno
24	34	70.8	10	19	AAW70085	E. coli methionyl-
25	34	70.8	16	22	AAG73122	Protease binding s
26	34	70.8	16	22	AAG73123	Protease binding s
27	34	70.8	16	22	AAG73124	Protease binding s
28	34	70.8	17	22	AAG73125	Protease binding s
29	34	70.8	18	22	AAG73126	Protease binding s
30	34	70.8	18	22	AAG73127	Protease binding s
31	34	70.8	18	22	AAG73128	Protease binding s
32	34	70.8	18	22	AAG73129	Protease binding
33	34	70.8	18	22	AAG73130	Protease binding s
34	34	70.8	18	22	AAG73235	Protease binding s
35	34	70.8	18	22	AAG73236	Protease binding s
36	34	70.8	18	22	AAG73237	Protease binding s
37	34	70.8	92	23	ABP09610	Human ORFX protein
38	34	70.8	122	21	AAB41270	Human ORFX ORF1034
39	34	70.8	122	23	ABP00694	Human ORFX protein
40	34	70.8	142	21	AAB40653	Human ORFX ORF417
41	34	70.8	205	19	AAY11083	H. pylori ORF 06ep
42	34	70.8	335	22	ABB58955	Drosophila melanog
43	34	70.8	387	22	ABB64800	Drosophila melanog
44	34	70.8	458	22	ABB71309	Drosophila melanog
45	34	70.8	471	22	ABG26200	Novel human diagno

ALIGNMENTS

RESULT 1
AAW54884
ID AAW54884 standard; peptide; 8 AA.
XX
AC AAW54884;
XX
DT 24-SEP-1998 (first entry)
XX
DE Isozyme-specific agonist peptide epsilon V1-7;E7.
XX
KW epsilon protein kinase C; ischaemic injury; hypoxic exposure.
XX
OS Synthetic.
XX
PN WO9817299-A1.
XX
PD 30-APR-1998.
XX
PF 17-OCT-1997; 97WO-US18716.
XX
PR 18-OCT-1996; 96US-0028724.
XX
PA (STRD) UNIV LELAND STANFORD JUNIOR.
XX
PI Mochly-Rosen D;
XX
DR WPI; 1998-261181/23.
XX
PT Peptide agonists of protein kinase C - used to reduce ischaemic
PT injury of cells exposed to hypoxic conditions
XX
PS Claim 1; Page 32; 47pp; English.
XX

```
CC   The peptides AAW54879-W54901 are agonists of epsilon protein kinase C
CC   (PKC).  They can be used for reducing ischaemic injury to a cell exposed
CC   to hypoxic conditions.  They can also be used in a method for
CC   identifying a compound effective to induce preconditioning.  The peptides
CC   are administered at a dose of 1-100 microgram administered once to
CC   several  times daily in bolus injections.
XX
SQ   Sequence   8 AA;

  Query Match             100.0%;  Score 48;  DB 19;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 7.8e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HDAPIGYD 8
          ||||||||
Db      1 HDAPIGYD 8


RESULT 2
AAW54889
ID   AAW54889 standard; peptide; 8 AA.
XX
AC   AAW54889;
XX
DT   24-SEP-1998  (first entry)
XX
DE   Isozyme-specific agonist peptide epsilon V1-7.5.
XX
KW   epsilon protein kinase C; ischaemic injury; hypoxic exposure.
XX
OS   Synthetic.
XX
PN   WO9817299-A1.
XX
PD   30-APR-1998.
XX
PF   17-OCT-1997;   97WO-US18716.
XX
PR   18-OCT-1996;   96US-0028724.
XX
PA   (STRD ) UNIV LELAND STANFORD JUNIOR.
XX
PI   Mochly-Rosen D;
XX
DR   WPI; 1998-261181/23.
XX
PT   Peptide agonists of protein kinase C - used to reduce ischaemic
PT   injury of cells exposed to hypoxic conditions
XX
PS   Disclosure; Page 32; 47pp; English.
XX
CC   The peptides AAW54879-W54901 are agonists of epsilon protein kinase C
CC   (PKC).  They can be used for reducing ischaemic injury to a cell exposed
CC   to hypoxic conditions.  They can also be used in a method for
CC   identifying a compound effective to induce preconditioning.  The peptides
CC   are administered at a dose of 1-100 microgram administered once to
CC   several  times daily in bolus injections.
XX
SQ   Sequence   8 AA;

  Query Match             89.6%;  Score 43;  DB 19;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 7.8e+05;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HDAPIGYD 8 .
          |:||||||
Db      1 HNAPIGYD 8


RESULT 3
AAW54892
ID   AAW54892 standard; peptide; 8 AA.
XX
AC   AAW54892;
XX
DT   24-SEP-1998  (first entry)
XX
DE   Isozyme-specific agonist peptide epsilon V1-7.8.
XX
KW   epsilon protein kinase C; ischaemic injury; hypoxic exposure.
XX
OS   Synthetic.
XX
PN   WO9817299-A1.
XX
PD   30-APR-1998.
XX
PF   17-OCT-1997;   97WO-US18716.
XX
PR   18-OCT-1996;   96US-0028724.
XX
PA   (STRD ) UNIV LELAND STANFORD JUNIOR.
XX
PI   Mochly-Rosen D;
XX
DR   WPI; 1998-261181/23.
XX
PT   Peptide agonists of protein kinase C - used to reduce ischaemic
PT   injury of cells exposed to hypoxic conditions
XX
PS   Claim 1; Page 32; 47pp; English.
XX
CC   The peptides AAW54879-W54901 are agonists of epsilon protein kinase C
CC   (PKC).  They can be used for reducing ischaemic injury to a cell exposed
CC   to hypoxic conditions.  They can also be used in a method for
CC   identifying a compound effective to induce preconditioning.  The peptides
CC   are administered at a dose of 1-100 microgram administered once to
CC   several  times daily in bolus injections.
XX
SQ   Sequence   8 AA;

  Query Match             89.6%;  Score 43;  DB 19;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 7.8e+05;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 HDAPIGYD 8
          |||| |||
Db      1 HDAPAGYD 8


RESULT 4
AAW54894
ID   AAW54894 standard; peptide; 8 AA.
XX
AC   AAW54894;
XX
DT   24-SEP-1998  (first entry)
XX
DE   Isozyme-specific agonist peptide epsilon V1-7.10.
XX
KW   epsilon protein kinase C; ischaemic injury; hypoxic exposure.
XX
OS   Synthetic.
XX
PN   WO9817299-A1.
XX
PD   30-APR-1998.
XX
PF   17-OCT-1997;   97WO-US18716.
XX
PR   18-OCT-1996;   96US-0028724.
XX
PA   (STRD ) UNIV LELAND STANFORD JUNIOR.
XX
PI   Mochly-Rosen D;
XX
```

```
DR   WPI; 1998-261181/23.
XX
PT   Peptide agonists of protein kinase C - used to reduce ischaemic
PT   injury of cells exposed to hypoxic conditions
XX
PS   Claim 1; Page 32; 47pp; English.
XX
CC   The peptides AAW54879-W54901 are agonists of epsilon protein kinase C
CC   (PKC).  They can be used for reducing ischaemic injury to a cell exposed
CC   to hypoxic conditions.  They can also be used in a method for
CC   identifying a compound effective to induce preconditioning.  The peptides
CC   are administered at a dose of 1-100 microgram administered once to
CC   several  times daily in bolus injections.
XX
SQ   Sequence   8 AA;

  Query Match             87.5%;  Score 42;  DB 19;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 7.8e+05;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 HDAPIGYD 8
          ||||| ||
Db      1 HDAPIAYD 8


RESULT 5
AAW54895
ID   AAW54895 standard; peptide; 8 AA.
XX
AC   AAW54895;
XX
DT   24-SEP-1998  (first entry)
XX
DE   Isozyme-specific agonist peptide epsilon V1-7.11.
XX
KW   epsilon protein kinase C; ischaemic injury; hypoxic exposure.
XX
OS   Synthetic.
XX
PN   WO9817299-A1.
XX
PD   30-APR-1998.
XX
PF   17-OCT-1997;   97WO-US18716.
XX
PR   18-OCT-1996;   96US-0028724.
XX
PA   (STRD ) UNIV LELAND STANFORD JUNIOR.
XX
PI   Mochly-Rosen D;
XX
DR   WPI; 1998-261181/23.
XX
PT   Peptide agonists of protein kinase C - used to reduce ischaemic
PT   injury of cells exposed to hypoxic conditions
XX
PS   Claim 1; Page 32; 47pp; English.
XX
CC   The peptides AAW54879-W54901 are agonists of epsilon protein kinase C
CC   (PKC).  They can be used for reducing ischaemic injury to a cell exposed
CC   to hypoxic conditions.  They can also be used in a method for
CC   identifying a compound effective to induce preconditioning.  The peptides
CC   are administered at a dose of 1-100 microgram administered once to
CC   several  times daily in bolus injections.
XX
SQ   Sequence   8 AA;

  Query Match             87.5%;  Score 42;  DB 19;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 7.8e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HDAPIGY 7
          |||||||
Db      1 HDAPIGY 7


RESULT 6
AAW17460
ID   AAW17460 standard; Peptide; 11 AA.
XX
AC   AAW17460;
XX
DT   31-OCT-1997  (first entry)
XX
DE   Protein kinase C-epsilon peptide delta V1-3 (81-91).
XX
KW   Signal transduction; cell signalling; modulator; immunomodulator;
KW   protein kinase C; receptor for activated kinase C; RACK;
KW   PKC-epsilon; cognate; graft rejection; autoimmune disease;
KW   allergy; asthma; therapy.
XX
OS   Homo sapiens.
XX
PN   WO9714038-A1.
XX
PD   17-APR-1997.
XX
PF   10-OCT-1996;   96WO-US16195.
XX
PR   18-JUN-1996;   96US-0665647.
PR   10-OCT-1995;   95US-0541964.
PR   31-JAN-1996;   96US-0594447.
XX
PA   (TERR-) TERRAPIN TECHNOLOGIES INC.
XX
PI   Kauvar LM,  Mochly-Rosen D,  Napolitano EW,  Ron D;
PI   Vasquez NJ,  Voronova A;
XX
DR   WPI; 1997-236030/21.
XX
PT   Identifying a modulator of intracellular signal transduction - by
PT   determining the interaction of a signal generating peptide with the
PT   test substance, allows modulation of the immune system
XX
PS   Claim 9; Page 32; 74pp; English.
XX
CC   This sequence is a peptide, designated epsilon V1-3, that
CC   corresponds to amino acid residues 81-91 in the V1 region of protein
CC   kinase C (PKC)-epsilon.  It is can be used as a signal generating
CC   peptide in a claimed method for identifying modulators of
CC   intracellular signal transduction.  This method assesses the ability
CC   of candidate modulators to affect the interaction between a signal-
CC   generating protein, such as a PKC isozyme peptide (see AAW15778-79,
CC   AAW15781, AAW15784-85, AAW17452-78), and a cognate binding protein
CC   involved in modulating the signal transduction function.  Identified
CC   substances are useful as immunomodulators (claimed).  They act to
CC   reduce T-cell activity, reduce the rate of graft rejection, reduce
CC   the severity of an autoimmune disorder, ameliorate allergy and/or
CC   asthma, or diminish a cytokine response (claimed).
XX
SQ   Sequence   11 AA;

  Query Match             87.5%;  Score 42;  DB 18;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0.11;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HDAPIGY 7
          |||||||
Db      5 HDAPIGY 11


RESULT 7
AAW54887
ID   AAW54887 standard; peptide; 8 AA.
XX
AC   AAW54887;
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XX
DT   24-SEP-1998  (first entry)
XX
DE   Isozyme-specific agonist peptide epsilon V1-7.3.
XX
KW   epsilon protein kinase C; ischaemic injury; hypoxic exposure.
XX
OS   Synthetic.
XX
PN   WO9817299-A1.
XX
PD   30-APR-1998.
XX
PF   17-OCT-1997;   97WO-US18716.
XX
PR   18-OCT-1996;   96US-0028724.
XX
PA   (STRD ) UNIV LELAND STANFORD JUNIOR.
XX
PI   Mochly-Rosen D;
XX
DR   WPI; 1998-261181/23.
XX
PT   Peptide agonists of protein kinase C - used to reduce ischaemic
PT   injury of cells exposed to hypoxic conditions
XX
PS   Claim 1; Page 32; 47pp; English.
XX
CC   The peptides AAW54879-W54901 are agonists of epsilon protein kinase C
CC   (PKC).  They can be used for reducing ischaemic injury to a cell exposed
CC   to hypoxic conditions.  They can also be used in a method for
CC   identifying a compound effective to induce preconditioning.  The peptides
CC   are administered at a dose of 1-100 microgram administered once to
CC   several  times daily in bolus injections.
XX
SQ   Sequence   8 AA;

  Query Match             83.3%;  Score 40;  DB 19;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 7.8e+05;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 HDAPIGYD 8
          ||| ||||
Db      1 HDAAIGYD 8


RESULT 8
AAW54888
ID   AAW54888 standard; peptide; 8 AA.
XX
AC   AAW54888;
XX
DT   24-SEP-1998  (first entry)
XX
DE   Isozyme-specific agonist peptide epsilon V1-7.4.
XX
KW   epsilon protein kinase C; ischaemic injury; hypoxic exposure.
XX
OS   Synthetic.
XX
PN   WO9817299-A1.
XX
PD   30-APR-1998.
XX
PF   17-OCT-1997;   97WO-US18716.
XX
PR   18-OCT-1996;   96US-0028724.
XX
PA   (STRD ) UNIV LELAND STANFORD JUNIOR.
XX
PI   Mochly-Rosen D;
XX
DR   WPI; 1998-261181/23.
XX
PT   Peptide agonists of protein kinase C - used to reduce ischaemic
PT   injury of cells exposed to hypoxic conditions
XX
PS   Claim 1; Page 32; 47pp; English.
XX
CC   The peptides AAW54879-W54901 are agonists of epsilon protein kinase C
CC   (PKC).  They can be used for reducing ischaemic injury to a cell exposed
CC   to hypoxic conditions.  They can also be used in a method for
CC   identifying a compound effective to induce preconditioning.  The peptides
CC   are administered at a dose of 1-100 microgram administered once to
CC   several  times daily in bolus injections.
XX
SQ   Sequence   8 AA;

  Query Match             83.3%;  Score 40;  DB 19;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 7.8e+05;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 HDAPIGYD 8
          ||||| ||
Db      1 HDAPIPYD 8


RESULT 9
AAW54890
ID   AAW54890 standard; peptide; 8 AA.
XX
AC   AAW54890;
XX
DT   24-SEP-1998  (first entry)
XX
DE   Isozyme-specific agonist peptide epsilon V1-7.6.
XX
KW   epsilon protein kinase C; ischaemic injury; hypoxic exposure.
XX
OS   Synthetic.
XX
PN   WO9817299-A1.
XX
PD   30-APR-1998.
XX
PF   17-OCT-1997;   97WO-US18716.
XX
PR   18-OCT-1996;   96US-0028724.
XX
PA   (STRD ) UNIV LELAND STANFORD JUNIOR.
XX
PI   Mochly-Rosen D;
XX
DR   WPI; 1998-261181/23.
XX
PT   Peptide agonists of protein kinase C - used to reduce ischaemic
PT   injury of cells exposed to hypoxic conditions
XX
PS   Claim 1; Page 32; 47pp; English.
XX
CC   The peptides AAW54879-W54901 are agonists of epsilon protein kinase C
CC   (PKC).  They can be used for reducing ischaemic injury to a cell exposed
CC   to hypoxic conditions.  They can also be used in a method for
CC   identifying a compound effective to induce preconditioning.  The peptides
CC   are administered at a dose of 1-100 microgram administered once to
CC   several  times daily in bolus injections.
XX
SQ   Sequence   8 AA;

  Query Match             83.3%;  Score 40;  DB 19;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 7.8e+05;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 HDAPIGYD 8
          | ||||||
Db      1 HAAPIGYD 8
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```
RESULT 10
AAW54891
ID   AAW54891 standard; peptide; 8 AA.
XX
AC   AAW54891;
XX
DT   24-SEP-1998  (first entry)
XX
DE   Isozyme-specific agonist peptide epsilon V1-7.7.
XX
KW   epsilon protein kinase C; ischaemic injury; hypoxic exposure.
XX
OS   Synthetic.
XX
PN   WO9817299-A1.
XX
PD   30-APR-1998.
XX
PF   17-OCT-1997;   97WO-US18716.
XX
PR   18-OCT-1996;   96US-0028724.
XX
PA   (STRD ) UNIV LELAND STANFORD JUNIOR.
XX
PI   Mochly-Rosen D;
XX
DR   WPI; 1998-261181/23.
XX
PT   Peptide agonists of protein kinase C - used to reduce ischaemic
PT   injury of cells exposed to hypoxic conditions
XX
PS   Claim 1; Page 32; 47pp; English.
XX
CC   The peptides AAW54879-W54901 are agonists of epsilon protein kinase C
CC   (PKC).  They can be used for reducing ischaemic injury to a cell exposed
CC   to hypoxic conditions.  They can also be used in a method for
CC   identifying a compound effective to induce preconditioning.  The peptides
CC   are administered at a dose of 1-100 microgram administered once to
CC   several  times daily in bolus injections.
XX
SQ   Sequence   8 AA;

  Query Match             83.3%;  Score 40;  DB 19;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 7.8e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 DAPIGYD 8
          |||||||
Db      2 DAPIGYD 8


RESULT 11
AAW54893
ID   AAW54893 standard; peptide; 8 AA.
XX
AC   AAW54893;
XX
DT   24-SEP-1998  (first entry)
XX
DE   Isozyme-specific agonist peptide epsilon V1-7.9.
XX
KW   epsilon protein kinase C; ischaemic injury; hypoxic exposure.
XX
OS   Synthetic.
XX
PN   WO9817299-A1.
XX
PD   30-APR-1998.
XX
PF   17-OCT-1997;   97WO-US18716.
XX
PR   18-OCT-1996;   96US-0028724.
XX
PA   (STRD ) UNIV LELAND STANFORD JUNIOR.
XX
PI   Mochly-Rosen D;
XX
DR   WPI; 1998-261181/23.
XX
PT   Peptide agonists of protein kinase C - used to reduce ischaemic
PT   injury of cells exposed to hypoxic conditions
XX
PS   Claim 1; Page 32; 47pp; English.
XX
CC   The peptides AAW54879-W54901 are agonists of epsilon protein kinase C
CC   (PKC).  They can be used for reducing ischaemic injury to a cell exposed
CC   to hypoxic conditions.  They can also be used in a method for
CC   identifying a compound effective to induce preconditioning.  The peptides
CC   are administered at a dose of 1-100 microgram administered once to
CC   several  times daily in bolus injections.
XX
SQ   Sequence   8 AA;

  Query Match             81.2%;  Score 39;  DB 19;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 7.8e+05;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 HDAPIGYD 8
          |||||| |
Db      1 HDAPIGAD 8


RESULT 12
AAW54898
ID   AAW54898 standard; peptide; 8 AA.
XX
AC   AAW54898;
XX
DT   24-SEP-1998  (first entry)
XX
DE   Isozyme-specific agonist peptide eta V1-7.
XX
KW   epsilon protein kinase C; ischaemic injury; hypoxic exposure.
XX
OS   Synthetic.
XX
PN   WO9817299-A1.
XX
PD   30-APR-1998.
XX
PF   17-OCT-1997;   97WO-US18716.
XX
PR   18-OCT-1996;   96US-0028724.
XX
PA   (STRD ) UNIV LELAND STANFORD JUNIOR.
XX
PI   Mochly-Rosen D;
XX
DR   WPI; 1998-261181/23.
XX
PT   Peptide agonists of protein kinase C - used to reduce ischaemic
PT   injury of cells exposed to hypoxic conditions
XX
PS   Disclosure; Page 32; 47pp; English.
XX
CC   The peptides AAW54879-W54901 are agonists of epsilon protein kinase C
CC   (PKC).  They can be used for reducing ischaemic injury to a cell exposed
CC   to hypoxic conditions.  They can also be used in a method for
CC   identifying a compound effective to induce preconditioning.  The peptides
CC   are administered at a dose of 1-100 microgram administered once to
CC   several  times daily in bolus injections.
XX
SQ   Sequence   8 AA;
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  Query Match             79.2%;  Score 38;  DB 19;  Length 8;
  Best Local Similarity   62.5%;  Pred. No. 7.8e+05;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 HDAPIGYD 8
           |: |:|||
Db       1 HETPLGYD 8


RESULT 13
AAW54901
ID   AAW54901 standard; peptide; 14 AA.
XX
AC   AAW54901;
XX
DT   24-SEP-1998  (first entry)
XX
DE   Isozyme-specific agonist peptide epsilon V1-7.1x.
XX
KW   epsilon protein kinase C; ischaemic injury; hypoxic exposure.
XX
OS   Synthetic.
XX
PN   WO9817299-A1.
XX
PD   30-APR-1998.
XX
PF   17-OCT-1997;   97WO-US18716.
XX
PR   18-OCT-1996;   96US-0028724.
XX
PA   (STRD ) UNIV LELAND STANFORD JUNIOR.
XX
PI   Mochly-Rosen D;
XX
DR   WPI; 1998-261181/23.
XX
PT   Peptide agonists of protein kinase C - used to reduce ischaemic
PT   injury of cells exposed to hypoxic conditions
XX
PS   Disclosure; Page 32; 47pp; English.
XX
CC   The peptides AAW54879-W54901 are agonists of epsilon protein kinase C
CC   (PKC).  They can be used for reducing ischaemic injury to a cell exposed
CC   to hypoxic conditions.  They can also be used in a method for
CC   identifying a compound effective to induce preconditioning.  The peptides
CC   are administered at a dose of 1-100 microgram administered once to
CC   several  times daily in bolus injections.
XX
SQ   Sequence   14 AA;

  Query Match             78.1%;  Score 37.5;  DB 19;  Length 14;
  Best Local Similarity   88.9%;  Pred. No. 1.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy       1 HDAPIG-YD 8
           |||||| ||
Db       4 HDAPIGDYD 12


RESULT 14
AAW54886
ID   AAW54886 standard; peptide; 6 AA.
XX
AC   AAW54886;
XX
DT   24-SEP-1998  (first entry)
XX
DE   Isozyme-specific agonist peptide epsilon V1-7.2.
XX
KW   epsilon protein kinase C; ischaemic injury; hypoxic exposure.
XX
OS   Synthetic.
XX
PN   WO9817299-A1.
XX
PD   30-APR-1998.
XX
PF   17-OCT-1997;   97WO-US18716.
XX
PR   18-OCT-1996;   96US-0028724.
XX
PA   (STRD ) UNIV LELAND STANFORD JUNIOR.
XX
PI   Mochly-Rosen D;
XX
DR   WPI; 1998-261181/23.
XX
PT   Peptide agonists of protein kinase C - used to reduce ischaemic
PT   injury of cells exposed to hypoxic conditions
XX
PS   Claim 1; Page 32; 47pp; English.
XX
CC   The peptides AAW54879-W54901 are agonists of epsilon protein kinase C
CC   (PKC).  They can be used for reducing ischaemic injury to a cell exposed
CC   to hypoxic conditions.  They can also be used in a method for
CC   identifying a compound effective to induce preconditioning.  The peptides
CC   are administered at a dose of 1-100 microgram administered once to
CC   several  times daily in bolus injections.
XX
SQ   Sequence   6 AA;

  Query Match             72.9%;  Score 35;  DB 19;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 7.8e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HDAPIG 6
           ||||||
Db       1 HDAPIG 6


RESULT 15
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ID   AAW54885 standard; peptide; 8 AA.
XX
AC   AAW54885;
XX
DT   24-SEP-1998  (first entry)
XX
DE   Isozyme-specific agonist peptide epsilon V1-7.1.
XX
KW   epsilon protein kinase C; ischaemic injury; hypoxic exposure.
XX
OS   Synthetic.
XX
PN   WO9817299-A1.
XX
PD   30-APR-1998.
XX
PF   17-OCT-1997;   97WO-US18716.
XX
PR   18-OCT-1996;   96US-0028724.
XX
PA   (STRD ) UNIV LELAND STANFORD JUNIOR.
XX
PI   Mochly-Rosen D;
XX
DR   WPI; 1998-261181/23.
XX
PT   Peptide agonists of protein kinase C - used to reduce ischaemic
PT   injury of cells exposed to hypoxic conditions
XX
PS   Claim 1; Page 32; 47pp; English.
XX
CC   The peptides AAW54879-W54901 are agonists of epsilon protein kinase C
CC   (PKC).  They can be used for reducing ischaemic injury to a cell exposed
```

CC to hypoxic conditions. They can also be used in a method for
CC identifying a compound effective to induce preconditioning. The peptides
CC are administered at a dose of 1-100 microgram administered once to
CC several times daily in bolus injections.
XX
SQ Sequence 8 AA;

Query Match 72.9%; Score 35; DB 19; Length 8;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIG 6
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Db 1 HDAPIG 6

Search completed: March 14, 2003, 09:22:00
Job time : 37 secs

GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: March 14, 2003, 09:21:09 ; Search time 14 Seconds
(without alignments)
16.813 Million cell updates/sec

Title: US-10-007-363-2
Perfect score: 48
Sequence: 1 HDAPIGYD 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	48	100.0	8	4	US-08-953-033-6	Sequence 6, Appli
2	43	89.6	8	4	US-08-953-033-11	Sequence 11, Appl
3	43	89.6	8	4	US-08-953-033-14	Sequence 14, Appl
4	42	87.5	8	4	US-08-953-033-16	Sequence 16, Appl
5	42	87.5	8	4	US-08-953-033-17	Sequence 17, Appl
6	42	87.5	11	1	US-08-594-447-19	Sequence 19, Appl
7	42	87.5	11	1	US-08-541-964-18	Sequence 18, Appl
8	42	87.5	11	2	US-08-665-647-33	Sequence 33, Appl
9	40	83.3	8	4	US-08-953-033-9	Sequence 9, Appli
10	40	83.3	8	4	US-08-953-033-10	Sequence 10, Appl
11	40	83.3	8	4	US-08-953-033-12	Sequence 12, Appl
12	40	83.3	8	4	US-08-953-033-13	Sequence 13, Appl
13	39	81.2	8	4	US-08-953-033-15	Sequence 15, Appl
14	38	79.2	8	4	US-08-953-033-20	Sequence 20, Appl
15	37.5	78.1	14	4	US-08-953-033-23	Sequence 23, Appl
16	35	72.9	6	4	US-08-953-033-8	Sequence 8, Appli
17	35	72.9	8	4	US-08-953-033-7	Sequence 7, Appli
18	35	72.9	649	4	US-09-134-001C-3891	Sequence 3891, Ap
19	34	70.8	10	1	US-08-584-226-22	Sequence 22, Appl
20	34	70.8	500	4	US-09-325-932A-149	Sequence 149, App
21	34	70.8	659	4	US-09-392-772-10	Sequence 10, Appl
22	33	68.8	262	2	US-08-602-359A-35	Sequence 35, Appl
23	32	66.7	11	1	US-08-594-447-26	Sequence 26, Appl
24	32	66.7	11	1	US-08-541-964-25	Sequence 25, Appl
25	32	66.7	11	2	US-08-665-647-40	Sequence 40, Appl
26	32	66.7	102	1	US-07-901-703-5	Sequence 5, Appli
27	32	66.7	102	1	US-08-278-729A-11	Sequence 11, Appl
28	32	66.7	102	1	US-08-155-343A-11	Sequence 11, Appl
29	32	66.7	102	1	US-08-406-672-11	Sequence 11, Appl
30	32	66.7	102	1	US-08-335-583C-50	Sequence 50, Appl
31	32	66.7	102	1	US-08-643-563A-11	Sequence 11, Appl
32	32	66.7	102	1	US-08-643-763A-11	Sequence 11, Appl
33	32	66.7	102	1	US-08-462-623-11	Sequence 11, Appl
34	32	66.7	102	1	US-08-451-953A-11	Sequence 11, Appl
35	32	66.7	102	2	US-08-445-468A-11	Sequence 11, Appl
36	32	66.7	102	2	US-08-461-397A-11	Sequence 11, Appl
37	32	66.7	102	2	US-08-912-088-11	Sequence 11, Appl
38	32	66.7	102	3	US-08-278-730A-11	Sequence 11, Appl
39	32	66.7	102	3	US-08-478-097A-6	Sequence 6, Appli
40	32	66.7	102	3	US-08-445-467-11	Sequence 11, Appl
41	32	66.7	102	3	US-08-480-515A-11	Sequence 11, Appl
42	32	66.7	102	4	US-08-414-033A-11	Sequence 11, Appl
43	32	66.7	102	4	US-08-271-556A-9	Sequence 9, Appli
44	32	66.7	102	4	US-08-931-858E-158	Sequence 158, App
45	32	66.7	102	4	US-08-981-739-158	Sequence 158, App

ALIGNMENTS

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RESULT 1
US-08-953-033-6
; Sequence 6, Application US/08953033
; Patent No. 6165977
;  GENERAL INFORMATION:
;    APPLICANT:  Mochly-Rosen, Daria
;    TITLE OF INVENTION:  ISOZYME-SPECIFIC ACTIVATORS
;    TITLE OF INVENTION:  OF PROTEIN KINASE C - METHODS AND COM
;    TITLE OF INVENTION:  POSITIONS
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  350 Cambridge Ave., Suite 250
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/953,033
;      FILING DATE:  17-OCT-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/028,724
;      FILING DATE:  18-OCT-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Petithory, Joanne R.
;      REGISTRATION NUMBER:  42,995
;      REFERENCE/DOCKET NUMBER:  8600-0174.30
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-324-0880
;      TELEFAX:  650-324-0960
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Other
;      LOCATION:  1...8
;      OTHER INFORMATION:  epsilon-PKC residues 85-92; epsilonV1-7; E7
US-08-953-033-6
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  Query Match             100.0%;  Score 48;  DB 4;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HDAPIGYD 8
           ||||||||
Db       1 HDAPIGYD 8


RESULT 2
US-08-953-033-11
; Sequence 11, Application US/08953033
; Patent No. 6165977
;  GENERAL INFORMATION:
;    APPLICANT:  Mochly-Rosen, Daria
;    TITLE OF INVENTION:  ISOZYME-SPECIFIC ACTIVATORS
;    TITLE OF INVENTION:  OF PROTEIN KINASE C - METHODS AND COM
;    TITLE OF INVENTION:  POSITIONS
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  350 Cambridge Ave., Suite 250
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/953,033
;      FILING DATE:  17-OCT-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/028,724
;      FILING DATE:  18-OCT-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Petithory, Joanne R.
;      REGISTRATION NUMBER:  42,995
;      REFERENCE/DOCKET NUMBER:  8600-0174.30
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-324-0880
;      TELEFAX:  650-324-0960
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Other
;      LOCATION:  1...8
;      OTHER INFORMATION:  epsilonV1-7.5
US-08-953-033-11

  Query Match             89.6%;  Score 43;  DB 4;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 1.9e+05;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HDAPIGYD 8
           |:||||||
Db       1 HNAPIGYD 8


RESULT 3
US-08-953-033-14
; Sequence 14, Application US/08953033
; Patent No. 6165977
;  GENERAL INFORMATION:
;    APPLICANT:  Mochly-Rosen, Daria
;    TITLE OF INVENTION:  ISOZYME-SPECIFIC ACTIVATORS
;    TITLE OF INVENTION:  OF PROTEIN KINASE C - METHODS AND COM
;    TITLE OF INVENTION:  POSITIONS
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  350 Cambridge Ave., Suite 250
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/953,033
;      FILING DATE:  17-OCT-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/028,724
;      FILING DATE:  18-OCT-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Petithory, Joanne R.
;      REGISTRATION NUMBER:  42,995
;      REFERENCE/DOCKET NUMBER:  8600-0174.30
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-324-0880
;      TELEFAX:  650-324-0960
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Other
;      LOCATION:  1...8
;      OTHER INFORMATION:  epsilonV1-7.8
US-08-953-033-14

  Query Match             89.6%;  Score 43;  DB 4;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 1.9e+05;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 HDAPIGYD 8
           |||| |||
Db       1 HDAPAGYD 8


RESULT 4
US-08-953-033-16
; Sequence 16, Application US/08953033
; Patent No. 6165977
;  GENERAL INFORMATION:
;    APPLICANT:  Mochly-Rosen, Daria
;    TITLE OF INVENTION:  ISOZYME-SPECIFIC ACTIVATORS
;    TITLE OF INVENTION:  OF PROTEIN KINASE C - METHODS AND COM
;    TITLE OF INVENTION:  POSITIONS
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  350 Cambridge Ave., Suite 250
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
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;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/953,033
;      FILING DATE:  17-OCT-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/028,724
;      FILING DATE:  18-OCT-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Petithory, Joanne R.
;      REGISTRATION NUMBER:  42,995
;      REFERENCE/DOCKET NUMBER:  8600-0174.30
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-324-0880
;      TELEFAX:  650-324-0960
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  No. 6165977e
;      LOCATION:  1...8
;      OTHER INFORMATION:  epsilonV1-7.10
US-08-953-033-16

  Query Match             87.5%;  Score 42;  DB 4;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 1.9e+05;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 HDAPIGYD 8
            ||||| ||
Db       1 HDAPIAYD 8


RESULT 5
US-08-953-033-17
; Sequence 17, Application US/08953033
; Patent No. 6165977
;  GENERAL INFORMATION:
;    APPLICANT:  Mochly-Rosen, Daria
;    TITLE OF INVENTION:  ISOZYME-SPECIFIC ACTIVATORS
;    TITLE OF INVENTION:  OF PROTEIN KINASE C - METHODS AND COM
;    TITLE OF INVENTION:  POSITIONS
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  350 Cambridge Ave., Suite 250
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/953,033
;      FILING DATE:  17-OCT-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/028,724
;      FILING DATE:  18-OCT-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Petithory, Joanne R.
;      REGISTRATION NUMBER:  42,995
;      REFERENCE/DOCKET NUMBER:  8600-0174.30
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-324-0880
;      TELEFAX:  650-324-0960
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  No. 6165977e
;      LOCATION:  1...8
;      OTHER INFORMATION:  epsilonV1-7.11
US-08-953-033-17

  Query Match             87.5%;  Score 42;  DB 4;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HDAPIGY 7
            |||||||
Db       1 HDAPIGY 7


RESULT 6
US-08-594-447-19
; Sequence 19, Application US/08594447
; Patent No. 5776716
;  GENERAL INFORMATION:
;    APPLICANT:  Ron, Dorit
;    APPLICANT:  Napolitano, Eugene W.
;    APPLICANT:  Voronova, Anna F.
;    TITLE OF INVENTION:  METHODS FOR IDENTIFYING AGENTS WHICH
;    TITLE OF INVENTION:  BLOCKTHE INTERACTION OF FYN WITH PKC-THETA, AND USES
;    TITLE OF INVENTION:  THEREOF
;    NUMBER OF SEQUENCES:  75
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  2000 Pennsylvania Avenue, NW - Ste. 5500
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1888
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/594,447
;      FILING DATE:  31-JAN-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  22550-20025.24
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 887-1500
;      TELEFAX:  (202) 822-0168
;      TELEX:  90-4030 MRSNFOERSWSH
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Peptide
;      LOCATION:  1..11
;      OTHER INFORMATION:  /label= epsilon-V1-3
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US-08-594-447-19

Query Match 87.5%; Score 42; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGY 7
|||||||
Db 5 HDAPIGY 11

RESULT 7
US-08-541-964-18
; Sequence 18, Application US/08541964
; Patent No. 5783405
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; APPLICANT: Kauvar, Lawrence M.
; APPLICANT: Napolitano, Eugene W.
; TITLE OF INVENTION: A RAPID SCREENING METHOD FOR EFFECTORS
; TITLE OF INVENTION: OF SIGNAL TRANSDUCTION
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW-STE. 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,964
; FILING DATE: 10-OCT-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22550-20025.23
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 822-0168
; TELEX: 90-4030 MRSNFOERSWSH
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..11
; OTHER INFORMATION: /label= epsilon-V1-3
US-08-541-964-18

Query Match 87.5%; Score 42; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGY 7
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Db 5 HDAPIGY 11

RESULT 8
US-08-665-647-33
; Sequence 33, Application US/08665647
; Patent No. 5935803
; GENERAL INFORMATION:
; APPLICANT: Dasquez, Nicki J.
; APPLICANT: Ron, Dorit
; APPLICANT: Voronova, Anna F.
; APPLICANT: Napolitano, Eugene W.
; TITLE OF INVENTION: METHODS TO IDENTIFY IMMUNOMODULATORS
; TITLE OF INVENTION: USING COGNATE INTERACTION OF PKC-THETA
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW - Ste. 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,647
; FILING DATE: 18-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22550-20025.25
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 822-0168
; TELEX: 90-4030 MRSNFOERSWSH
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..11
; OTHER INFORMATION: /label= epsilon-V1-3
US-08-665-647-33

Query Match 87.5%; Score 42; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGY 7
|||||||
Db 5 HDAPIGY 11

RESULT 9
US-08-953-033-9
; Sequence 9, Application US/08953033
; Patent No. 6165977
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: ISOZYME-SPECIFIC ACTIVATORS
; TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM
; TITLE OF INVENTION: POSITIONS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

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;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ for Windows Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/953,033
;       FILING DATE:  17-OCT-1997
;       CLASSIFICATION:  530
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  60/028,724
;       FILING DATE:  18-OCT-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Petithory, Joanne R.
;       REGISTRATION NUMBER:  42,995
;       REFERENCE/DOCKET NUMBER:  8600-0174.30
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  650-324-0880
;       TELEFAX:  650-324-0960
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  9:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  8 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     FEATURE:
;       NAME/KEY:  Other
;       LOCATION:  1...8
;       OTHER INFORMATION:  epsilonV1-7.3
US-08-953-033-9

  Query Match             83.3%;  Score 40;  DB 4;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 1.9e+05;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 HDAPIGYD 8
          ||| ||||
Db      1 HDAAIGYD 8


RESULT 10
US-08-953-033-10
; Sequence 10, Application US/08953033
; Patent No. 6165977
;  GENERAL INFORMATION:
;     APPLICANT:  Mochly-Rosen, Daria
;     TITLE OF INVENTION:  ISOZYME-SPECIFIC ACTIVATORS
;     TITLE OF INVENTION:  OF PROTEIN KINASE C - METHODS AND COM
;     TITLE OF INVENTION:  POSITIONS
;     NUMBER OF SEQUENCES:  23
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Dehlinger & Associates
;       STREET:  350 Cambridge Ave., Suite 250
;       CITY:  Palo Alto
;       STATE:  CA
;       COUNTRY:  USA
;       ZIP:  94306
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ for Windows Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/953,033
;       FILING DATE:  17-OCT-1997
;       CLASSIFICATION:  530
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  60/028,724
;       FILING DATE:  18-OCT-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Petithory, Joanne R.
;       REGISTRATION NUMBER:  42,995
;       REFERENCE/DOCKET NUMBER:  8600-0174.30
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  650-324-0880
;       TELEFAX:  650-324-0960
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  10:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  8 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     FEATURE:
;       NAME/KEY:  Other
;       LOCATION:  1...8
;       OTHER INFORMATION:  epsilonV1-7.4
US-08-953-033-10

  Query Match             83.3%;  Score 40;  DB 4;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 1.9e+05;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 HDAPIGYD 8
          ||||| ||
Db      1 HDAPIPYD 8


RESULT 11
US-08-953-033-12
; Sequence 12, Application US/08953033
; Patent No. 6165977
;  GENERAL INFORMATION:
;     APPLICANT:  Mochly-Rosen, Daria
;     TITLE OF INVENTION:  ISOZYME-SPECIFIC ACTIVATORS
;     TITLE OF INVENTION:  OF PROTEIN KINASE C - METHODS AND COM
;     TITLE OF INVENTION:  POSITIONS
;     NUMBER OF SEQUENCES:  23
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Dehlinger & Associates
;       STREET:  350 Cambridge Ave., Suite 250
;       CITY:  Palo Alto
;       STATE:  CA
;       COUNTRY:  USA
;       ZIP:  94306
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ for Windows Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/953,033
;       FILING DATE:  17-OCT-1997
;       CLASSIFICATION:  530
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  60/028,724
;       FILING DATE:  18-OCT-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Petithory, Joanne R.
;       REGISTRATION NUMBER:  42,995
;       REFERENCE/DOCKET NUMBER:  8600-0174.30
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  650-324-0880
;       TELEFAX:  650-324-0960
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  12:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  8 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     FEATURE:
;       NAME/KEY:  Other
;       LOCATION:  1...8
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;      OTHER INFORMATION:  epsilonV1-7.6
US-08-953-033-12

  Query Match             83.3%;  Score 40;  DB 4;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 1.9e+05;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 HDAPIGYD 8
          | ||||||
Db      1 HAAPIGYD 8


RESULT 12
US-08-953-033-13
; Sequence 13, Application US/08953033
; Patent No. 6165977
;  GENERAL INFORMATION:
;    APPLICANT:  Mochly-Rosen, Daria
;    TITLE OF INVENTION:  ISOZYME-SPECIFIC ACTIVATORS
;    TITLE OF INVENTION:  OF PROTEIN KINASE C - METHODS AND COM
;    TITLE OF INVENTION:  POSITIONS
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  350 Cambridge Ave., Suite 250
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/953,033
;      FILING DATE:  17-OCT-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/028,724
;      FILING DATE:  18-OCT-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Petithory, Joanne R.
;      REGISTRATION NUMBER:  42,995
;      REFERENCE/DOCKET NUMBER:  8600-0174.30
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-324-0880
;      TELEFAX:  650-324-0960
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Other
;      LOCATION:  1...8
;      OTHER INFORMATION:  epsilonV1-7.7
US-08-953-033-13

  Query Match             83.3%;  Score 40;  DB 4;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 DAPIGYD 8
          |||||||
Db      2 DAPIGYD 8


RESULT 13
US-08-953-033-15
; Sequence 15, Application US/08953033
; Patent No. 6165977
;  GENERAL INFORMATION:
;    APPLICANT:  Mochly-Rosen, Daria
;    TITLE OF INVENTION:  ISOZYME-SPECIFIC ACTIVATORS
;    TITLE OF INVENTION:  OF PROTEIN KINASE C - METHODS AND COM
;    TITLE OF INVENTION:  POSITIONS
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  350 Cambridge Ave., Suite 250
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/953,033
;      FILING DATE:  17-OCT-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/028,724
;      FILING DATE:  18-OCT-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Petithory, Joanne R.
;      REGISTRATION NUMBER:  42,995
;      REFERENCE/DOCKET NUMBER:  8600-0174.30
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-324-0880
;      TELEFAX:  650-324-0960
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Other
;      LOCATION:  1...8
;      OTHER INFORMATION:  epsilonV1-7.9
US-08-953-033-15

  Query Match             81.2%;  Score 39;  DB 4;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 1.9e+05;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 HDAPIGYD 8
          ||||||
Db      1 HDAPIGAD 8


RESULT 14
US-08-953-033-20
; Sequence 20, Application US/08953033
; Patent No. 6165977
;  GENERAL INFORMATION:
;    APPLICANT:  Mochly-Rosen, Daria
;    TITLE OF INVENTION:  ISOZYME-SPECIFIC ACTIVATORS
;    TITLE OF INVENTION:  OF PROTEIN KINASE C - METHODS AND COM
;    TITLE OF INVENTION:  POSITIONS
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dehlinger & Associates
;      STREET:  350 Cambridge Ave., Suite 250
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
```

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;       ZIP:  94306
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ for Windows Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/953,033
;       FILING DATE:  17-OCT-1997
;       CLASSIFICATION:  530
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  60/028,724
;       FILING DATE:  18-OCT-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Petithory, Joanne R.
;       REGISTRATION NUMBER:  42,995
;       REFERENCE/DOCKET NUMBER:  8600-0174.30
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  650-324-0880
;       TELEFAX:  650-324-0960
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  20:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  8 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     FEATURE:
;       NAME/KEY:  Other
;       LOCATION:  1...8
;       OTHER INFORMATION:  nV1-7
US-08-953-033-20

  Query Match             79.2%;  Score 38;  DB 4;  Length 8;
  Best Local Similarity   62.5%;  Pred. No. 1.9e+05;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 HDAPIGYD 8
            |: |:|||
Db       1 HETPLGYD 8


RESULT 15
US-08-953-033-23
; Sequence 23, Application US/08953033
; Patent No. 6165977
;  GENERAL INFORMATION:
;     APPLICANT:  Mochly-Rosen, Daria
;     TITLE OF INVENTION:  ISOZYME-SPECIFIC ACTIVATORS
;     TITLE OF INVENTION:  OF PROTEIN KINASE C - METHODS AND COM
;     TITLE OF INVENTION:  POSITIONS
;     NUMBER OF SEQUENCES:  23
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Dehlinger & Associates
;       STREET:  350 Cambridge Ave., Suite 250
;       CITY:  Palo Alto
;       STATE:  CA
;       COUNTRY:  USA
;       ZIP:  94306
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ for Windows Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/953,033
;       FILING DATE:  17-OCT-1997
;       CLASSIFICATION:  530
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  60/028,724
;       FILING DATE:  18-OCT-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Petithory, Joanne R.
;       REGISTRATION NUMBER:  42,995
;       REFERENCE/DOCKET NUMBER:  8600-0174.30
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  650-324-0880
;       TELEFAX:  650-324-0960
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  23:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  14 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     FEATURE:
;       NAME/KEY:  Other
;       LOCATION:  1...14
;       OTHER INFORMATION:  epsilonV1-7.1x
US-08-953-033-23

  Query Match             78.1%;  Score 37.5;  DB 4;  Length 14;
  Best Local Similarity   88.9%;  Pred. No. 0.33;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy       1 HDAPIG-YD 8
            ||||||  ||
Db       4 HDAPIGDYD 12


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GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

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(without alignments)
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Title: US-10-007-363-2
Perfect score: 48
Sequence: 1 HDAPIGYD 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 199416 seqs, 46092074 residues

Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
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14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	48	100.0	8	9	US-10-007-363-2	Sequence 2, Appli
2	48	100.0	156	10	US-09-771-161A-104	Sequence 104, App
3	48	100.0	737	10	US-09-771-161A-195	Sequence 195, App
4	44	91.7	8	9	US-10-007-363-7	Sequence 7, Appli
5	44	91.7	8	9	US-10-007-363-13	Sequence 13, Appl
6	43	89.6	8	9	US-10-007-363-8	Sequence 8, Appli
7	42	87.5	8	9	US-10-007-363-9	Sequence 9, Appli
8	40	83.3	8	9	US-10-007-363-12	Sequence 12, Appl
9	40	83.3	8	9	US-10-007-363-14	Sequence 14, Appl
10	36	75.0	8	9	US-10-007-363-6	Sequence 6, Appli
11	36	75.0	8	9	US-10-007-363-17	Sequence 17, Appl
12	35	72.9	8	9	US-10-007-363-10	Sequence 10, Appl
13	35	72.9	8	9	US-10-007-363-11	Sequence 11, Appl
14	35	72.9	287	10	US-09-925-301-1386	Sequence 1386, Ap
15	34	70.8	550	10	US-09-841-132-562	Sequence 562, App
16	34	70.8	560	10	US-09-841-132-492	Sequence 492, App
17	34	70.8	677	10	US-09-815-242-10210	Sequence 10210, A
18	34	70.8	677	10	US-09-815-242-11921	Sequence 11921, A
19	34	70.8	682	10	US-09-815-242-11214	Sequence 11214, A
20	34	70.8	704	10	US-09-815-242-13925	Sequence 13925, A
21	34	70.8	1131	10	US-09-801-368-72	Sequence 72, Appl
22	33	68.8	262	9	US-10-027-805-35	Sequence 35, Appl
23	33	68.8	262	10	US-09-903-410-35	Sequence 35, Appl
24	32	66.7	118	12	US-10-115-406-15	Sequence 15, Appl
25	32	66.7	138	10	US-09-925-297-879	Sequence 879, App
26	32	66.7	143	12	US-10-002-278-4	Sequence 4, Appli
27	32	66.7	472	9	US-09-981-353-11	Sequence 11, Appl
28	32	66.7	472	10	US-09-841-758-1	Sequence 1, Appli
29	32	66.7	472	10	US-09-841-758-3	Sequence 3, Appli
30	32	66.7	499	10	US-09-925-300-1717	Sequence 1717, Ap
31	32	66.7	575	10	US-09-220-091-7	Sequence 7, Appli
32	32	66.7	648	10	US-09-815-242-10504	Sequence 10504, A
33	32	66.7	896	9	US-09-903-170C-5	Sequence 5, Appli
34	32	66.7	896	10	US-09-903-180B-5	Sequence 5, Appli
35	32	66.7	896	10	US-09-903-171A-5	Sequence 5, Appli
36	32	66.7	896	10	US-09-903-188A-5	Sequence 5, Appli
37	32	66.7	896	10	US-09-903-323A-5	Sequence 5, Appli
38	32	66.7	896	10	US-09-903-325A-5	Sequence 5, Appli
39	32	66.7	979	10	US-09-903-187A-5	Sequence 5, Appli
40	31	64.6	8	9	US-10-007-363-16	Sequence 16, Appl
41	31	64.6	142	10	US-09-815-242-13015	Sequence 13015,
42	31	64.6	294	10	US-09-815-242-13076	Sequence 13076, A
43	31	64.6	472	10	US-09-841-758-4	Sequence 4, Appli
44	31	64.6	493	9	US-09-738-626-4893	Sequence 4893, Ap
45	31	64.6	690	10	US-09-815-242-5841	Sequence 5841, Ap

ALIGNMENTS

RESULT 1
US-10-007-363-2
; Sequence 2, Application US/10007363
; Patent No. US20020168354A1
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
; TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to
; TITLE OF INVENTION: Ischemia
; FILE REFERENCE: 58600-8209.US00
; CURRENT APPLICATION NUMBER: US/10/007,363
; CURRENT FILING DATE: 2002-11-09
; PRIOR APPLICATION NUMBER: US 60/247,830
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pseudo-epsilon RACK octapeptide
US-10-007-363-2

Query Match 100.0%; Score 48; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
||||||||
Db 1 HDAPIGYD 8

RESULT 2
US-09-771-161A-104
; Sequence 104, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS Of PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A

```
;  CURRENT FILING DATE:  2001-01-26
;  PRIOR APPLICATION NUMBER: 09/724,676
;  PRIOR FILING DATE: 2000-11-28
;  PRIOR APPLICATION NUMBER: 136776
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 135619
;  PRIOR FILING DATE: 2000-04-12
;  NUMBER OF SEQ ID NOS: 273
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 104
;   LENGTH: 156
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-771-161A-104

  Query Match           100.0%;  Score 48;  DB 10;  Length 156;
  Best Local Similarity  100.0%;  Pred. No. 0.019;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HDAPIGYD 8
          ||||||||
Db     85 HDAPIGYD 92


RESULT 3
US-09-771-161A-195
; Sequence 195, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
;  APPLICANT: LEVINE, et al.
;  TITLE OF INVENTION: VARIANTS Of PROTEIN KINASES
;  FILE REFERENCE: 802620-2005.1
;  CURRENT APPLICATION NUMBER: US/09/771,161A
;  CURRENT FILING DATE:  2001-01-26
;  PRIOR APPLICATION NUMBER: 09/724,676
;  PRIOR FILING DATE: 2000-11-28
;  PRIOR APPLICATION NUMBER: 136776
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 135619
;  PRIOR FILING DATE: 2000-04-12
;  NUMBER OF SEQ ID NOS: 273
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 195
;   LENGTH: 737
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-771-161A-195

  Query Match           100.0%;  Score 48;  DB 10;  Length 737;
  Best Local Similarity  100.0%;  Pred. No. 0.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HDAPIGYD 8
          ||||||||
Db     85 HDAPIGYD 92


RESULT 4
US-10-007-363-7
; Sequence 7, Application US/10007363
; Patent No. US20020168354A1
; GENERAL INFORMATION:
;  APPLICANT: Mochly-Rosen, Daria
;  TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
;  TITLE OF INVENTION:  and Method for Protection Against Tissue Damage Due to
;  TITLE OF INVENTION:  Ischemia
;  FILE REFERENCE: 58600-8209.US00
;  CURRENT APPLICATION NUMBER: US/10/007,363
;  CURRENT FILING DATE:  2002-11-09
;  PRIOR APPLICATION NUMBER: US 60/247,830
;  PRIOR FILING DATE: 2000-11-10
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: modified pseudo-epsilon RACK peptide
US-10-007-363-7

  Query Match           91.7%;  Score 44;  DB 9;  Length 8;
  Best Local Similarity  87.5%;  Pred. No. 1.7e+05;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HDAPIGYD 8
          |:|||||:
Db      1 HDAPIGYE 8


RESULT 5
US-10-007-363-13
; Sequence 13, Application US/10007363
; Patent No. US20020168354A1
; GENERAL INFORMATION:
;  APPLICANT: Mochly-Rosen, Daria
;  TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
;  TITLE OF INVENTION:  and Method for Protection Against Tissue Damage Due to
;  TITLE OF INVENTION:  Ischemia
;  FILE REFERENCE: 58600-8209.US00
;  CURRENT APPLICATION NUMBER: US/10/007,363
;  CURRENT FILING DATE:  2002-11-09
;  PRIOR APPLICATION NUMBER: US 60/247,830
;  PRIOR FILING DATE: 2000-11-10
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: modified pseudo-epsilon RACK peptide
US-10-007-363-13

  Query Match           91.7%;  Score 44;  DB 9;  Length 8;
  Best Local Similarity  87.5%;  Pred. No. 1.7e+05;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 HDAPIGYD 8
          || |||||
Db      1 HDGPIGYD 8


RESULT 6
US-10-007-363-8
; Sequence 8, Application US/10007363
; Patent No. US20020168354A1
; GENERAL INFORMATION:
;  APPLICANT: Mochly-Rosen, Daria
;  TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
;  TITLE OF INVENTION:  and Method for Protection Against Tissue Damage Due to
;  TITLE OF INVENTION:  Ischemia
;  FILE REFERENCE: 58600-8209.US00
;  CURRENT APPLICATION NUMBER: US/10/007,363
;  CURRENT FILING DATE:  2002-11-09
;  PRIOR APPLICATION NUMBER: US 60/247,830
;  PRIOR FILING DATE: 2000-11-10
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: modified pseudo-epsilon RACK peptide
US-10-007-363-8
```

```
  Query Match             89.6%;  Score 43;  DB 9;  Length 8;
  Best Local Similarity   75.0%;  Pred. No. 1.7e+05;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HDAPIGYD 8
          ||||:||:
Db      1 HDAPVGYE 8


RESULT 7
US-10-007-363-9
; Sequence 9, Application US/10007363
; Patent No. US20020168354A1
; GENERAL INFORMATION:
;  APPLICANT: Mochly-Rosen, Daria
;  TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
;  TITLE OF INVENTION:  and Method for Protection Against Tissue Damage Due to
;  TITLE OF INVENTION:  Ischemia
;  FILE REFERENCE: 58600-8209.US00
;  CURRENT APPLICATION NUMBER: US/10/007,363
;  CURRENT FILING DATE:  2002-11-09
;  PRIOR APPLICATION NUMBER: US 60/247,830
;  PRIOR FILING DATE: 2000-11-10
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: modified pseudo-epsilon RACK peptide
US-10-007-363-9

  Query Match             87.5%;  Score 42;  DB 9;  Length 8;
  Best Local Similarity   75.0%;  Pred. No. 1.7e+05;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HDAPIGYD 8
          ||||:||:
Db      1 HDAPLGYE 8


RESULT 8
US-10-007-363-12
; Sequence 12, Application US/10007363
; Patent No. US20020168354A1
; GENERAL INFORMATION:
;  APPLICANT: Mochly-Rosen, Daria
;  TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
;  TITLE OF INVENTION:  and Method for Protection Against Tissue Damage Due to
;  TITLE OF INVENTION:  Ischemia
;  FILE REFERENCE: 58600-8209.US00
;  CURRENT APPLICATION NUMBER: US/10/007,363
;  CURRENT FILING DATE:  2002-11-09
;  PRIOR APPLICATION NUMBER: US 60/247,830
;  PRIOR FILING DATE: 2000-11-10
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: modified pseudo-epsilon RACK peptide
US-10-007-363-12

  Query Match             83.3%;  Score 40;  DB 9;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 DAPIGYD 8
          |||||||
Db      2 DAPIGYD 8


RESULT 9
US-10-007-363-14
; Sequence 14, Application US/10007363
; Patent No. US20020168354A1
; GENERAL INFORMATION:
;  APPLICANT: Mochly-Rosen, Daria
;  TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
;  TITLE OF INVENTION:  and Method for Protection Against Tissue Damage Due to
;  TITLE OF INVENTION:  Ischemia
;  FILE REFERENCE: 58600-8209.US00
;  CURRENT APPLICATION NUMBER: US/10/007,363
;  CURRENT FILING DATE:  2002-11-09
;  PRIOR APPLICATION NUMBER: US 60/247,830
;  PRIOR FILING DATE: 2000-11-10
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: modified pseudo-epsilon RACK peptide
US-10-007-363-14

  Query Match             83.3%;  Score 40;  DB 9;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 1.7e+05;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 HDAPIGYD 8
          ||| ||||
Db      1 HDAAIGYD 8


RESULT 10
US-10-007-363-6
; Sequence 6, Application US/10007363
; Patent No. US20020168354A1
; GENERAL INFORMATION:
;  APPLICANT: Mochly-Rosen, Daria
;  TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
;  TITLE OF INVENTION:  and Method for Protection Against Tissue Damage Due to
;  TITLE OF INVENTION:  Ischemia
;  FILE REFERENCE: 58600-8209.US00
;  CURRENT APPLICATION NUMBER: US/10/007,363
;  CURRENT FILING DATE:  2002-11-09
;  PRIOR APPLICATION NUMBER: US 60/247,830
;  PRIOR FILING DATE: 2000-11-10
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: modified pseudo-epsilon RACK peptide
US-10-007-363-6

  Query Match             75.0%;  Score 36;  DB 9;  Length 8;
  Best Local Similarity   75.0%;  Pred. No. 1.7e+05;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 HDAPIGYD 8
          |:| ||||
Db      1 HEADIGYD 8


RESULT 11
US-10-007-363-17
; Sequence 17, Application US/10007363
; Patent No. US20020168354A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: Mochly-Rosen, Daria
;  TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
;  TITLE OF INVENTION:  and Method for Protection Against Tissue Damage Due to
;  TITLE OF INVENTION:  Ischemia
;  FILE REFERENCE: 58600-8209.US00
;  CURRENT APPLICATION NUMBER: US/10/007,363
;  CURRENT FILING DATE:  2002-11-09
;  PRIOR APPLICATION NUMBER: US 60/247,830
;  PRIOR FILING DATE: 2000-11-10
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: modified pseudo-epsilon RACK peptide
US-10-007-363-17

  Query Match             75.0%;  Score 36;  DB 9;  Length 8;
  Best Local Similarity   75.0%;  Pred. No. 1.7e+05;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 HDAPIGYD 8
          ||  ||||
Db      1 HDGDIGYD 8


RESULT 12
US-10-007-363-10
; Sequence 10, Application US/10007363
; Patent No. US20020168354A1
; GENERAL INFORMATION:
;  APPLICANT: Mochly-Rosen, Daria
;  TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
;  TITLE OF INVENTION:  and Method for Protection Against Tissue Damage Due to
;  TITLE OF INVENTION:  Ischemia
;  FILE REFERENCE: 58600-8209.US00
;  CURRENT APPLICATION NUMBER: US/10/007,363
;  CURRENT FILING DATE:  2002-11-09
;  PRIOR APPLICATION NUMBER: US 60/247,830
;  PRIOR FILING DATE: 2000-11-10
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: modified pseudo-epsilon RACK peptide
US-10-007-363-10

  Query Match             72.9%;  Score 35;  DB 9;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HDAPIG 6
          ||||||
Db      1 HDAPIG 6


RESULT 13
US-10-007-363-11
; Sequence 11, Application US/10007363
; Patent No. US20020168354A1
; GENERAL INFORMATION:
;  APPLICANT: Mochly-Rosen, Daria
;  TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
;  TITLE OF INVENTION:  and Method for Protection Against Tissue Damage Due to
;  TITLE OF INVENTION:  Ischemia
;  FILE REFERENCE: 58600-8209.US00
;  CURRENT APPLICATION NUMBER: US/10/007,363
;  CURRENT FILING DATE:  2002-11-09
;  PRIOR APPLICATION NUMBER: US 60/247,830
;  PRIOR FILING DATE: 2000-11-10
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: modified pseudo-epsilon RACK peptide
US-10-007-363-11

  Query Match             72.9%;  Score 35;  DB 9;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HDAPIG 6
          ||||||
Db      1 HDAPIG 6


RESULT 14
US-09-925-301-1386
; Sequence 1386, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA106
;  CURRENT APPLICATION NUMBER: US/09/925,301
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05882
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 1694
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1386
;   LENGTH: 287
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-925-301-1386

  Query Match             72.9%;  Score 35;  DB 10;  Length 287;
  Best Local Similarity   75.0%;  Pred. No. 14;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 HDAPIGYD 8
          ||  ||| |
Db     16 HDIPIGID 23


RESULT 15
US-09-841-132-562
; Sequence 562, Application US/09841132
; Patent No. US20020061848A1
; GENERAL INFORMATION:
;  APPLICANT: Bhatia, Ajay
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Probst, Peter
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
;  TITLE OF INVENTION:  DIAGNOSIS OF CHLAMYDIAL INFECTION
;  FILE REFERENCE: 210121.469C8
;  CURRENT APPLICATION NUMBER: US/09/841,132
;  CURRENT FILING DATE:  2001-04-23
;  NUMBER OF SEQ ID NOS: 599
;  SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 562
;   LENGTH: 550
;   TYPE: PRT
;   ORGANISM: C. Trachomatis D serovar
US-09-841-132-562
```

Query Match 70.8%; Score 34; DB 10; Length 550;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2 DAPIGY 7
           ||||||
Db     253 DAPIGY 258
```

Search completed: March 14, 2003, 09:23:46
Job time : 14 secs

GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: March 14, 2003, 09:19:59 ; Search time 17 Seconds
(without alignments)
45.240 Million cell updates/sec

Title: US-10-007-363-2
Perfect score: 48
Sequence: 1 HDAPIGYD 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	48	100.0	736	1	KIRBCE	protein kinase C (
2	48	100.0	737	1	S28942	protein kinase C (
3	48	100.0	737	1	KIRTCE	protein kinase C (
4	48	100.0	737	1	KIMSCE	protein kinase C (
5	39	81.2	652	2	T39409	hypothetical prote
6	39	81.2	869	1	JC4858	VLDL receptor prec
7	38	79.2	682	1	A39666	protein kinase C (
8	38	79.2	683	1	A23690	protein kinase (EC
9	38	79.2	683	1	S29478	protein kinase C (
10	38	79.2	1025	2	T10259	RNA-directed DNA p
11	37	77.1	2203	2	T42742	voltage-dependent
12	35	72.9	180	2	T47414	hypothetical prote
13	35	72.9	199	2	AC3241	conserved hypothet
14	35	72.9	371	2	T26389	hypothetical prote
15	35	72.9	400	2	T41569	hypothetical prote
16	35	72.9	457	2	JC5422	FK506-binding prot
17	35	72.9	468	2	S45145	H+-transporting tw
18	35	72.9	471	1	S14733	H+-transporting tw
19	35	72.9	471	2	H84363	H+-transporting AT
20	35	72.9	699	2	A38368	chitinase (EC 3.2.
21	35	72.9	1023	2	A47296	thiazide-sensitive
22	34.5	71.9	553	2	T06499	Rieske [2Fe-2S] ir
23	34	70.8	205	2	D71918	hypothetical prote
24	34	70.8	290	2	S36706	B4 protein - equin
25	34	70.8	304	2	T42554	tegument protein -
26	34	70.8	312	2	T50960	related to nodulat
27	34	70.8	326	2	T29810	hypothetical prote
28	34	70.8	326	2	JS0169	collagen col-14 -
29	34	70.8	392	2	AB2474	hypothetical prote
30	34	70.8	411	2	A96985	uncharacterized co
31	34	70.8	423	2	E64157	hypothetical prote
32	34	70.8	432	2	B65190	potassium uptake p
33	34	70.8	483	2	A91226	potassium uptake p
34	34	70.8	483	2	G86072	potassium uptake p
35	34	70.8	483	2	AB0458	Trk system potassi
36	34	70.8	547	2	D84942	methionine-tRNA li
37	34	70.8	550	2	H81718	methionyl-tRNA syn
38	34	70.8	550	2	C71567	methionine-tRNA li
39	34	70.8	551	2	H81552	methionyl-tRNA syn
40	34	70.8	551	2	C86506	methionyl-tRNA syn
41	34	70.8	551	2	H72117	methionine-tRNA li
42	34	70.8	658	2	D69431	methionine-tRNA li
43	34	70.8	675	2	AF0185	methionine-tRNA li
44	34	70.8	677	1	SYECMT	methionine-tRNA li
45	34	70.8	677	2	H90993	methionine tRNA sy

ALIGNMENTS

RESULT 1
KIRBCE
protein kinase C (EC 2.7.1.-) epsilon - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 21-Nov-1997
C;Accession: A29880
R;Ohno, S.; Akita, Y.; Konno, Y.; Imajoh, S.; Suzuki, K.
Cell 53, 731-741, 1988
A;Title: A novel phorbol ester receptor/protein kinase, nPKC, distantly related to tl
A;Reference number: A29880; MUID:88223367; PMID:3370672
A;Accession: A29880
A;Molecule type: mRNA
A;Residues: 1-736 <OHN>
A;Cross-references: GB:M20014
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threc
A;Note: activity is calcium-independent, phospholipid-dependent, and activated by dia
C;Superfamily: protein kinase C delta; protein kinase C zinc-binding repeat homology;
C;Keywords: ATP; autophosphorylation; duplication; phorbol ester binding; phospholipi
F;156-161/Region: pseudophosphorylation motif
F;170-220/Domain: protein kinase C zinc-binding repeat homology <KZ1>
F;243-292/Domain: protein kinase C zinc-binding repeat homology <KZ2>
F;405-667/Domain: protein kinase homology <KIN>
F;413-421/Region: protein kinase ATP-binding motif
F;170,201,204,220/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F;183,186,209,212/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F;243,273,276,292/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F;256,259,281,284/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F;436,455,531,533/Active site: Lys, Glu, Asp, Lys #status predicted
F;702,709/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status p

Query Match 100.0%; Score 48; DB 1; Length 736;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 HDAPIGYD 8
           ||||||||
Db      85 HDAPIGYD 92
```

RESULT 2
S28942
protein kinase C (EC 2.7.1.-) epsilon - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 11-Jun-1999
C;Accession: S28942
R;Basta, P.; Strickland, M.B.; Holmes, W.; Loomis, C.R.; Ballas, L.M.; Burns, D.J.
Biochim. Biophys. Acta 1132, 154-160, 1992
A;Title: Sequence and expression of human protein kinase C-epsilon.
A;Reference number: S28942; MUID:93003318; PMID:1382605
A;Accession: S28942
A;Status: preliminary

A;Molecule type: mRNA
A;Residues: 1-737 <BAS>
A;Cross-references: EMBL:X65293; NID:g35494; PIDN:CAA46388.1; PID:g35495
C;Comment: This is a calcium-independent, phospholipid-dependent, serine- and threonine-
of inositol phospholipids. This protein is a receptor for tumor-promoting phorbol ester
C;Genetics:
A;Gene: GDB:PRKCE
A;Cross-references: GDB:128039; OMIM:176975
A;Map position: 3pter-3qter
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A;Note: activity is calcium-independent, phospholipid-dependent, and activated by diacyl
C;Superfamily: protein kinase C delta; protein kinase C zinc-binding repeat homology; pr
C;Keywords: ATP; duplication; phorbol ester binding; phospholipid binding; phosphotransf
F;156-161/Region: pseudophosphorylation motif
F;170-220/Domain: protein kinase C zinc-binding repeat homology <KZ1>
F;243-292/Domain: protein kinase C zinc-binding repeat homology <KZ2>
F;406-668/Domain: protein kinase homology <KIN>
F;414-422/Region: protein kinase ATP-binding motif
F;170,201,204,220/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F;183,186,209,212/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F;243,273,276,292/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F;256,259,281,284/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F;437,456,532,534/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 100.0%; Score 48; DB 1; Length 737;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
||||||||
Db 85 HDAPIGYD 92

RESULT 3
KIRTCE
protein kinase C (EC 2.7.1.-) epsilon - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
C;Accession: B28163; B26408; S00216
R;Ono, Y.; Fujii, T.; Ogita, K.; Kikkawa, U.; Igarashi, K.; Nishizuka, Y.
J. Biol. Chem. 263, 6927-6932, 1988
A;Title: The structure, expression, and properties of additional members of the protein
A;Reference number: A92717; MUID:88198270; PMID:2834397
A;Accession: B28163
A;Molecule type: DNA
A;Residues: 1-737 <ONO>
A;Cross-references: GB:M18331; NID:g206182; PIDN:AAA41872.1; PID:g206183
R;Housey, G.M.; O'Brian, C.A.; Johnson, M.D.; Kirschmeier, P.; Weinstein, I.B.
Proc. Natl. Acad. Sci. U.S.A. 84, 1065-1069, 1987
A;Title: Isolation of cDNA clones encoding protein kinase C: evidence for a protein kina
A;Reference number: A94145; MUID:87147193; PMID:3469647
A;Accession: B26408
A;Molecule type: mRNA
A;Residues: 397-447,'GQRGLHDDREEDFGSGAET',467,'LSNPTLLLLPDQGPPLLRQ',487-545,'C',547-636
A;Cross-references: GB:M15523; NID:g206192; PIDN:AAA41877.1; PID:g206193
C;Comment: Protein kinase C epsilon and epsilon' appear to be encoded by the same gene a
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A;Note: activity is calcium-independent, phospholipid-dependent, and activated by diacyl
C;Superfamily: protein kinase C delta; protein kinase C zinc-binding repeat homology; pr
C;Keywords: alternative splicing; ATP; autophosphorylation; duplication; phorbol ester b
C
F;156-161/Region: pseudophosphorylation motif
F;170-220/Domain: protein kinase C zinc-binding repeat homology <KZ1>
F;243-292/Domain: protein kinase C zinc-binding repeat homology <KZ2>
F;406-668/Domain: protein kinase homology <KIN>
F;414-422/Region: protein kinase ATP-binding motif
F;170,201,204,220/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F;183,186,209,212/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F;243,273,276,292/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F;256,259,281,284/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F;437,456,532,534/Active site: Lys, Glu, Asp, Lys #status predicted
F;703,710/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status p

Query Match 100.0%; Score 48; DB 1; Length 737;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
||||||||
Db 85 HDAPIGYD 92

RESULT 4
KIMSCE
protein kinase C (EC 2.7.1.-) epsilon - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 21-Nov-1997
C;Accession: S02270
R;Schaap, D.; Parker, P.J.; Bristol, A.; Kriz, R.; Knopf, J.
FEBS Lett. 243, 351-357, 1989
A;Title: Unique substrate specificity and regulatory properties of PKC-epsilon:
A;Reference number: S02270; MUID:89137541; PMID:2917656
A;Accession: S02270
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-737 <SCH>
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threo
A;Note: activity is calcium-independent, phospholipid-dependent, and activated by dia
C;Superfamily: protein kinase C delta; protein kinase C zinc-binding repeat homology;
C;Keywords: ATP; autophosphorylation; duplication; phorbol ester binding; phospholipi
F;156-161/Region: pseudophosphorylation motif
F;170-220/Domain: protein kinase C zinc-binding repeat homology <KZ1>
F;243-292/Domain: protein kinase C zinc-binding repeat homology <KZ2>
F;406-668/Domain: protein kinase homology <KIN>
F;414-422/Region: protein kinase ATP-binding motif
F;170,201,204,220/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F;183,186,209,212/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F;243,273,276,292/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F;256,259,281,284/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F;437,456,532,534/Active site: Lys, Glu, Asp, Lys #status predicted
F;703,710/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status p

Query Match 100.0%; Score 48; DB 1; Length 737;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HDAPIGYD 8
||||||||
Db 85 HDAPIGYD 92

RESULT 5
T39409
hypothetical protein SPBC13G1.08c - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T39409
R;Lyne, M.; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Badcock, K.; Churcher, C.M.
submitted to the EMBL Data Library, April 1998
A;Reference number: Z21852
A;Accession: T39409
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-652 <LYN>
A;Cross-references: EMBL:AL022600; PIDN:CAA18661.1; GSPDB:GN00067; SPDB:SPBC13G1.08c
A;Experimental source: strain 972h-; cosmid c13G1
C;Genetics:
A;Gene: SPDB:SPBC13G1.08c
A;Map position: 2

Query Match 81.2%; Score 39; DB 2; Length 652;
Best Local Similarity 85.7%; Pred. No. 7.4;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy      2 DAPIGYD 8
          |||:|||
Db    419 DAPVGYD 425


RESULT 6
JC4858
VLDL receptor precursor - African clawed frog
N;Alternate names: very low density lipoprotein receptor; vitellogenin receptor
C;Species: Xenopus laevis (African clawed frog)
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 16-Jun-2000
C;Accession: JC4858
R;Okabayashi, K.; Shoji, H.; Nakamura, T.; Hashimoto, O.; Asashima, M.; Sugino, H.
Biochem. Biophys. Res. Commun. 224, 406-413, 1996
A;Title: cDNA cloning and expression of the Xenopus laevis vitellogenin receptor.
A;Reference number: JC4858; MUID:96295501; PMID:8702402
A;Accession: JC4858
A;Molecule type: mRNA
A;Residues: 1-869 <OKA>
A;Cross-references: GB:AB006906; NID:g2366772; PIDN:BAA22145.1; PID:g2366773
C;Comment: This receptor mediates incorporation of vitellogenin into oocytes.
C;Superfamily: LDL receptor; EGF homology; LDL receptor ligand-binding repeat homology;
C;Keywords: duplication; fatty acid metabolism; glycoprotein; receptor; transmembrane pr
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-869/Product: VLDL receptor #status predicted <MAT>
F;27-793/Domain: extracellular #status predicted <EXT>
F;32-66/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;71-107/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;112-148/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F;153-187/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F;192-228/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F;238-272/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F;277-311/Domain: LDL receptor ligand-binding repeat homology <LDL7>
F;317-354/Domain: LDL receptor ligand-binding repeat homology <LDL8>
F;359-393/Domain: EGF homology <EG1>
F;399-433/Domain: EGF homology <EG2>
F;440-479/Domain: LDL receptor YWTD-containing repeat homology <YW1>
F;480-525/Domain: LDL receptor YWTD-containing repeat homology <YW2>
F;526-568/Domain: LDL receptor YWTD-containing repeat homology <YW3>
F;569-612/Domain: LDL receptor YWTD-containing repeat homology <YW4>
F;613-655/Domain: LDL receptor YWTD-containing repeat homology <YW5>
F;656-698/Domain: LDL receptor YWTD-containing repeat homology <YW6>
F;707-749/Domain: EGF homology <EG3>
F;794-815/Domain: transmembrane #status predicted <TMM>
F;816-869/Domain: intracellular #status predicted <CYT>
F;830-834/Region: coated-pit mediated internalization signal
F;150,201,777,786/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;359-370,366-379,381-393,399-409,405-418,420-433,707-720,716-735,737-749/Disulfide bond

  Query Match             81.2%;  Score 39;  DB 1;  Length 869;
  Best Local Similarity   75.0%;  Pred. No. 10;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 HDAPIGYD 8
          || ||||:
Db    371 HDLPIGYE 378


RESULT 7
A39666
protein kinase C (EC 2.7.1.-) eta - human
N;Alternate names: protein kinase C PKC-L
C;Species: Homo sapiens (man)
C;Date: 08-Nov-1991 #sequence_revision 11-Apr-1997 #text_change 21-Jul-2000
C;Accession: A39666; A42131; S65018
R;Bacher, N.; Zisman, Y.; Berent, E.; Livneh, E.
Mol. Cell. Biol. 11, 126-133, 1991
A;Title: Isolation and characterization of PKC-L, a new member of the protein kinase C-r
A;Reference number: A39666; MUID:91094824; PMID:1986216
A;Accession: A39666
A;Molecule type: mRNA
A;Residues: 1-276,'YVNECAY','SMSSERG',292-296,'MRWN',301,'PRP','GRD',309-682 <BA2>
A;Cross-references: GB:M55284; NID:g189988; PIDN:AAA60100.1; PID:g189989
A;Note: the cross-reference is to the corrected sequence
R;Bacher, N.; Zisman, Y.; Berent, E.; Livneh, E.
Mol. Cell. Biol. 12, 1404, 1992
A;Title: Isolation and characterization of PKC-L, a new member of the protein kinase
A;Reference number: A42131; MUID:92186874; PMID:1545821
A;Contents: erratum
A;Accession: A42131
A;Molecule type: mRNA
A;Residues: 277-308 <BA3>
A;Cross-references: GB:M55284
A;Note: this report is a revision to reference A39666
R;Palmer, R.H.; Ridden, J.; Parker, P.J.
FEBS Lett. 356, 5-8, 1994
A;Title: Identification of multiple, novel, protein kinase C-related gene products.
A;Reference number: S51020; MUID:95080426; PMID:7988719
A;Accession: S65018
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 437-470,'E',472-538 <PAL>
A;Cross-references: EMBL:S74620; NID:g786485; PIDN:AAB32724.1; PID:g786486
C;Genetics:
A;Gene: GDB:PRKCH; PKC-L; PRKCL
A;Cross-references: GDB:129009
A;Map position: 19q13.4-19q13.4
C;Function:
A;Description: catalyzes protein phosphorylation at Ser or Thr residues
A;Note: activity is calcium-independent, phospholipid-dependent, and activated by di
C;Superfamily: protein kinase C delta; protein kinase C zinc-binding repeat homology
C;Keywords: ATP; autophosphorylation; duplication; phorbol ester binding; phospholip
F;157-162/Region: pseudophosphorylation motif
F;171-221/Domain: protein kinase C zinc-binding repeat homology <KZ1>
F;245-294/Domain: protein kinase C zinc-binding repeat homology <KZ2>
F;352-613/Domain: protein kinase homology <KIN>
F;360-368/Region: protein kinase ATP-binding motif
F;171,202,205,221/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F;184,187,210,213/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F;245,275,278,294/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F;258,261,283,286/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F;383,402,478,480/Active site: Lys, Glu, Asp, Lys #status predicted

  Query Match             79.2%;  Score 38;  DB 1;  Length 682;
  Best Local Similarity   62.5%;  Pred. No. 12;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 HDAPIGYD 8
          |: |:|||
Db     88 HETPLGYD 95


RESULT 8
A23690
protein kinase (EC 2.7.1.37) eta - mouse
C;Species: Mus musculus (house mouse)
C;Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change 16-Jun-2000
C;Accession: A23690
R;Osada, S.; Mizuno, K.; Saido, T.C.; Akita, Y.; Suzuki, K.; Kuroki, T.; Ohno, S.
J. Biol. Chem. 265, 22434-22440, 1990
A;Title: A phorbol ester receptor/protein kinase, nPKC-eta, a new member of the prot
A;Reference number: A23690; MUID:91093089; PMID:2266135
A;Accession: A23690
A;Molecule type: mRNA
A;Residues: 1-683 <OSA>
A;Cross-references: GB:D90242; GB:J05703; NID:g220526; PIDN:BAA14288.1; PID:g220527
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-thre
A;Note: activity is calcium-independent, phospholipid-dependent, and activated by di
C;Superfamily: protein kinase C delta; protein kinase C zinc-binding repeat homology
C;Keywords: ATP; autophosphorylation; duplication; phorbol ester binding; phospholip
F;158-163/Region: pseudophosphorylation motif
F;172-222/Domain: protein kinase C zinc-binding repeat homology <KZ1>
F;246-295/Domain: protein kinase C zinc-binding repeat homology <KZ2>
F;353-614/Domain: protein kinase homology <KIN>
```

```
F;361-369/Region: protein kinase ATP-binding motif
F;172,203,206,222/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F;185,188,211,214/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F;246,276,279,295/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F;259,262,284,287/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F;384,403,479,481/Active site: Lys, Glu, Asp, Lys #status predicted

  Query Match             79.2%;  Score 38;  DB 1;  Length 683;
  Best Local Similarity   62.5%;  Pred. No. 12;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 HDAPIGYD 8
            |: |:|||
Db      88 HETPLGYD 95


RESULT 9
S29478
protein kinase C (EC 2.7.1.-) eta - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 11-Jun-1999
C;Accession: I60246; S29478
R;Dekker, L.V.; Parker, P.J.; McIntyre, P.
FEBS Lett. 312, 195-199, 1992
A;Title: Biochemical properties of rat protein kinase C-eta expressed in COS cells.
A;Reference number: I60246; MUID:93050193; PMID:1426252
A;Accession: I60246
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-683 <RES>
A;Cross-references: EMBL:X68400; NID:g56915; PIDN:CAA48466.1; PID:g56916
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonir
A;Note: activity is calcium-independent, phospholipid-dependent, and activated by diacyl
C;Superfamily: protein kinase C delta; protein kinase C zinc-binding repeat homology; pr
C;Keywords: ATP; autophosphorylation; duplication; phorbol ester binding; phospholipid b
F;158-163/Region: pseudophosphorylation motif
F;172-222/Domain: protein kinase C zinc-binding repeat homology <KZ1>
F;246-295/Domain: protein kinase C zinc-binding repeat homology <KZ2>
F;353-614/Domain: protein kinase homology <KIN>
F;361-369/Region: protein kinase ATP-binding motif
F;172,203,206,222/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F;185,188,211,214/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F;246,276,279,295/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F;259,262,284,287/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F;384,403,479,481/Active site: Lys, Glu, Asp, Lys #status predicted

  Query Match             79.2%;  Score 38;  DB 1;  Length 683;
  Best Local Similarity   62.5%;  Pred. No. 12;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 HDAPIGYD 8
            |: |:|||
Db      88 HETPLGYD 95


RESULT 10
T10259
RNA-directed DNA polymerase (EC 2.7.7.49) - pteromalid wasp (Nasonia vitripennis) retrot
C;Species: Nasonia vitripennis
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T10259; I44490
R;Burke, W.D.; Malik, H.S.; Lathe III, W.C.; Eickbush, T.H.
Nature 392, 141-142, 1998
A;Title: Are retrotransposons long-term hitchhikers?.
A;Reference number: Z17001; MUID:98175715; PMID:9515960
A;Accession: T10259
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1025 <BUR>
A;Cross-references: EMBL:L00950; NID:g3559783; PIDN:AAC34927.1; PID:g2317818
R;Burke, W.D.; Eickbush, D.G.; Xiong, Y.; Jakubczak, J.; Eickbush, T.H.
Mol. Biol. Evol. 10, 163-185, 1993
A;Title: Sequence relationship of retrotransposable elements R1 and R2 within and bet
A;Reference number: A44490; MUID:93196484; PMID:8383793
A;Contents: retrotransposable element R2
A;Accession: I44490
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 314-956,'Q','A',971,'AA' <BU2>
A;Note: sequence extracted from NCBI backbone (NCBIP:127243)
C;Genetics:
A;Mobile element: retrotransposon R2
C;Keywords: nucleotidyltransferase

  Query Match             79.2%;  Score 38;  DB 2;  Length 1025;
  Best Local Similarity   85.7%;  Pred. No. 19;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 HDAPIGY 7
            || ||||
Db     709 HDTPIGY 715


RESULT 11
T42742
voltage-dependent calcium channel alpha 1 chain, isoform CACN4A - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
C;Accession: T42742
R;Ihara, Y.; Yamada, Y.; Fujii, Y.; Gonori, T.; Yano, H.; Yasuda, K.; Inagaki, N.; Se
Mol. Endocrinol. 9, 121-130, 1995
A;Title: Molecular diversity and functional characterization of voltage-dependent cal
A;Reference number: Z22258; MUID:95280950; PMID:7760845
A;Accession: T42742
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2203 <IHA>
A;Cross-references: EMBL:D38101; NID:g736711; PIDN:BAA07282.1; PID:g736712
A;Experimental source: insulinoma RINm5F complementary DNA library
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain
C;Keywords: calcium channel

  Query Match             77.1%;  Score 37;  DB 2;  Length 2203;
  Best Local Similarity   85.7%;  Pred. No. 70;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 DAPIGYD 8
            |:|||||
Db    1937 DSPIGYD 1943


RESULT 12
T47414
hypothetical protein T28A8.70 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T47414
R;Purnelle, B.; Boutry, M.; Goffeau, A.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.
submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24466
A;Accession: T47414
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-180 <PUR>
A;Cross-references: EMBL:AL162691
A;Experimental source: cultivar Columbia: BAC clone T28A8
C;Genetics:
A;Map position: 3
A;Introns: 21/2; 32/2; 91/3; 105/3
A;Note: T28A8.70

  Query Match             72.9%;  Score 35;  DB 2;  Length 180;
  Best Local Similarity   75.0%;  Pred. No. 12;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
```

```
Qy      1 HDAPIGYD 8
            || ||| |
Db     38 HDIPIGVD 45
```

RESULT 13
AC3241
conserved hypothetical protein Atu6109 [imported] - Agrobacterium tumefaciens (strain C5
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C;Accession: AC3241
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:11743193
A;Accession: AC3241
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-199 <KUR>
A;Cross-references: GB:AE008690; PIDN:AAL46345.1; PID:g17744134; GSPDB:GN00189
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu6109
A;Genome: plasmid

  Query Match 72.9%; Score 35; DB 2; Length 199;
  Best Local Similarity 71.4%; Pred. No. 13;
  Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy      2 DAPIGYD 8
          | |:|||
Db    127 DGPVGYD 133
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RESULT 14
T26389
hypothetical protein Y105C5B.m - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26389
R;McMurray, A.
submitted to the EMBL Data Library, September 1999
A;Reference number: Z20208
A;Accession: T26389
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-371 <WIL>
A;Cross-references: EMBL:AL110479; NID:e1542153; PIDN:CAB54361.1; CESP:Y105C5B.m
A;Experimental source: clone Y105C5B
C;Genetics:
A;Gene: CESP:Y105C5B.m
A;Introns: 24/1; 56/1; 101/3; 138/2; 219/3; 290/3; 332/2

  Query Match 72.9%; Score 35; DB 2; Length 371;
  Best Local Similarity 85.7%; Pred. No. 26;
  Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      2 DAPIGYD 8
          | |||||
Db     59 DLPIGYD 65
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RESULT 15
T41569
hypothetical protein SPCC736.12c - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T41569
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.
submitted to the EMBL Data Library, May 1998
A;Reference number: Z21991
A;Accession: T41569
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-400 <WOO>
A;Cross-references: EMBL:AL023705; PIDN:CAA19276.1; GSPDB:GN00068; SPDB:SPCC736.12c
A;Experimental source: strain 972h-; cosmid c736
C;Genetics:
A;Gene: SPDB:SPCC736.12c
A;Map position: 3
A;Introns: 29/1; 349/1

  Query Match 72.9%; Score 35; DB 2; Length 400;
  Best Local Similarity 100.0%; Pred. No. 29;
  Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 HDAPIG 6
          ||||||
Db     76 HDAPIG 81
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Search completed: March 14, 2003, 09:22:26
Job time : 19 secs

GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: March 14, 2003, 09:16:54 ; Search time 12 Seconds
(without alignments)
27.651 Million cell updates/sec

Title: US-10-007-363-2
Perfect score: 48
Sequence: 1 HDAPIGYD 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	48	100.0	736	1	KPCE_RABIT	P10830 oryctolagus
2	48	100.0	737	1	KPCE_HUMAN	Q02156 homo sapien
3	48	100.0	737	1	KPCE_MOUSE	P16054 mus musculu
4	48	100.0	737	1	KPCE_RAT	P09216 rattus norv
5	38	79.2	682	1	KPCL_HUMAN	P24723 homo sapien
6	38	79.2	683	1	KPCL_MOUSE	P23298 mus musculu
7	38	79.2	683	1	KPCL_RAT	Q64617 rattus norv
8	38	79.2	1025	1	PO21_NASVI	Q03278 nasonia vit
9	37	77.1	2203	1	CCAD_RAT	P27732 rattus norv
10	35	72.9	456	1	FKB5_MOUSE	Q64378 mus musculu
11	35	72.9	457	1	FKB5_HUMAN	Q13451 h 51 kda fk
12	35	72.9	468	1	VATB_HALVO	Q48333 halobacteri
13	35	72.9	471	1	VATB_HALN1	Q9hne4 halobacteri
14	35	72.9	471	1	VATB_HALSA	P25164 halobacteri
15	35	72.9	699	1	CHI1_BACCI	P20533 bacillus ci
16	35	72.9	1023	1	TSCC_PSEAM	P55019 pseudopleur
17	34	70.8	290	1	UL49_HSVE4	Q00039 equine herp
18	34	70.8	345	1	CC14_CAEEL	P18834 caenorhabdi
19	34	70.8	483	1	TRKH_ECOLI	P21166 escherichia
20	34	70.8	487	1	TRKH_HAEIN	P44843 haemophilus
21	34	70.8	547	1	SYM_BUCAI	P57210 buchnera ap
22	34	70.8	550	1	SYM_CHLMU	Q9pl07 chlamydia m
23	34	70.8	550	1	SYM_CHLTR	O84035 chlamydia t
24	34	70.8	551	1	SYM_CHLPN	Q9z959 chlamydia p
25	34	70.8	658	1	SYM_ARCFU	O28819 archaeoglob
26	34	70.8	676	1	SYM_ECOLI	P00959 escherichia
27	34	70.8	682	1	SYM_HAEIN	P43828 haemophilus
28	34	70.8	682	1	SYM_PASMU	P57838 pasteurella
29	34	70.8	734	1	SYM_BORBU	Q44951 borrelia bu
30	34	70.8	797	1	SYM_ARATH	Q9svn5 arabidopsis
31	34	70.8	804	1	SYM_ORYSA	Q9ztsl oryza sativ
32	34	70.8	917	1	SYM_CAEEL	Q20970 caenorhabdi
33	34	70.8	1131	1	CHS1_YEAST	P08004 saccharomyc
34	33	68.8	156	1	CU55_ARADI	P80518 araneus dia
35	33	68.8	483	1	TRKH_SALTY	Q91612 salmonella
36	33	68.8	554	1	RECN_VIBCH	P52118 vibrio chol
37	33	68.8	811	1	SYM_TREPA	O83776 treponema p
38	32	66.7	139	1	YS87_MYCTU	Q10810 mycobacteri
39	32	66.7	307	1	UFD1_MOUSE	P70362 mus musculu
40	32	66.7	319	1	K6PF_LACDE	P80019 lactobacill
41	32	66.7	324	1	THI4_FUSSH	P23617 fusarium so
42	32	66.7	343	1	UFD1_HUMAN	Q92890 homo sapien
43	32	66.7	372	1	DECA_TRICA	Q26974 tribolium c
44	32	66.7	472	1	SBP1_HUMAN	Q13228 homo sapien
45	32	66.7	581	1	AMY1_SCHPO	Q09840 schizosacch

ALIGNMENTS

RESULT 1
KPCE_RABIT
ID KPCE_RABIT STANDARD; PRT; 736 AA.
AC P10830;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Protein kinase C, epsilon type (EC 2.7.1.-) (nPKC-epsilon).
GN PRKCE.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88223367; PubMed=3370672;
RA Ohno S., Akita Y., Konno Y., Imajoh S., Suzuki K.;
RT "A novel phorbol ester receptor/protein kinase, nPKC, distantly
RT related to the protein kinase C family.";
RL Cell 53:731-741(1988).
CC -!- FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC -!- SIMILARITY: CONTAINS 2 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
CC BINDING DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC ----------

CC ----------
DR EMBL; M20014; AAA31426.1; -.
DR PIR; A29880; KIRBCE.
DR HSSP; P28867; 1PTQ.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00130; DAG_PE-bind; 2.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.

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DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS50004; C2_DOMAIN_2; 1.
DR   PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR   PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   Repeat; ATP-binding; Transferase; Phosphorylation;
KW   Serine/threonine-protein kinase; Phorbol-ester binding; Zinc.
FT   DOMAIN        1     99       C2 DOMAIN.
FT   DOMAIN      170    220       PHORBOL-ESTER AND DAG BINDING 1.
FT   DOMAIN      243    292       PHORBOL-ESTER AND DAG BINDING 2.
FT   DOMAIN      407    667       PROTEIN KINASE.
FT   NP_BIND     413    421       ATP (BY SIMILARITY).
FT   BINDING     436    436       ATP (BY SIMILARITY).
FT   ACT_SITE    531    531       BY SIMILARITY.
FT   MOD_RES     702    702       PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT   MOD_RES     709    709       PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ   SEQUENCE   736 AA;  83515 MW;  261C4FEE59E9BFEB CRC64;

  Query Match             100.0%;  Score 48;  DB 1;  Length 736;
  Best Local Similarity   100.0%;  Pred. No. 0.033;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HDAPIGYD 8
          ||||||||
Db     85 HDAPIGYD 92


RESULT 2
KPCE_HUMAN
ID   KPCE_HUMAN     STANDARD;      PRT;   737 AA.
AC   Q02156; Q9UE81;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Protein kinase C, epsilon type (EC 2.7.1.-) (nPKC-epsilon).
GN   PRKCE OR PKCE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93003318; PubMed=1382605;
RA   Basta P., Strickland M.B., Holmes W., Loomis C.R., Ballas L.M.,
RA   Burns D.J.;
RT   "Sequence and expression of human protein kinase C-epsilon.";
RL   Biochim. Biophys. Acta 1132:154-160(1992).
RN   [2]
RP   SEQUENCE OF 1-116 FROM N.A.
RA   Waterston R.;
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-DEPENDENT,
CC       SERINE- AND THREONINE-SPECIFIC ENZYME.
CC   -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC       PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC       THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC   -!- SIMILARITY: CONTAINS 2 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
CC       BINDING DOMAINS.
CC   -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC       PKC SUBFAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X65293; CAA46388.1; -.
DR   EMBL; U51244; AAD08855.1; -.
DR   PIR; S28942; S28942.
DR   HSSP; P28867; 1PTQ.
DR   Genew; HGNC:9401; PRKCE.
DR   MIM; 176975; -.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR002219; DAG_PE-bind.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR000961; Pkinase_C.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   Pfam; PF00130; DAG_PE-bind; 2.
DR   Pfam; PF00168; C2; 1.
DR   Pfam; PF00433; pkinase_C; 1.
DR   PRINTS; PR00008; DAGPEDOMAIN.
DR   ProDom; PD000001; Euk_pkinase; 1.
DR   SMART; SM00109; C1; 2.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00133; S_TK_X; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS50004; C2_DOMAIN_2; 1.
DR   PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR   PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   Repeat; ATP-binding; Transferase; Phosphorylation;
KW   Serine/threonine-protein kinase; Phorbol-ester binding; Zinc.
FT   DOMAIN        1     99       C2 DOMAIN.
FT   DOMAIN      170    220       PHORBOL-ESTER AND DAG BINDING 1.
FT   DOMAIN      243    292       PHORBOL-ESTER AND DAG BINDING 2.
FT   DOMAIN      408    668       PROTEIN KINASE.
FT   NP_BIND     414    422       ATP (BY SIMILARITY).
FT   BINDING     437    437       ATP (BY SIMILARITY).
FT   ACT_SITE    532    532       BY SIMILARITY.
FT   MOD_RES     703    703       PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT   MOD_RES     710    710       PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ   SEQUENCE   737 AA;  83673 MW;  85032D0A091A1F7F CRC64;

  Query Match             100.0%;  Score 48;  DB 1;  Length 737;
  Best Local Similarity   100.0%;  Pred. No. 0.033;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HDAPIGYD 8
          ||||||||
Db     85 HDAPIGYD 92


RESULT 3
KPCE_MOUSE
ID   KPCE_MOUSE     STANDARD;      PRT;   737 AA.
AC   P16054;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Protein kinase C, epsilon type (EC 2.7.1.-) (nPKC-epsilon).
GN   PRKCE OR PKCE OR PKCEA.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89137541; PubMed=2917656;
RA   Schaap D., Parker P.J., Bristol A., Kriz R., Knopf J.;
RT   "Unique substrate specificity and regulatory properties of
RT   PKC-epsilon: a rationale for diversity.";
RL   FEBS Lett. 243:351-357(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=98127436; PubMed=9467942;
RA   Wang Q.J., Acs P., Goodnight J., Blumberg P.M., Mischak H.,
```

```
RA   Mushinski J.F.;
RT   "The catalytic domain of PKC-epsilon, in reciprocal PKC-delta and -
RT   epsilon chimeras, is responsible for conferring tumorgenicity to
RT   NIH3T3 cells, whereas both regulatory and catalytic domains of
RT   PKC-epsilon contribute to in vitro transformation.";
RL   Oncogene 16:53-60(1998).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Wheeler D.L.;
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-DEPENDENT,
CC       SERINE- AND THREONINE-SPECIFIC ENZYME.
CC   -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC       PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC       THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC   -!- SIMILARITY: CONTAINS 2 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
CC       BINDING DOMAINS.
CC   -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC       PKC SUBFAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF028009; AAB84189.1; -.
DR   EMBL; AF325507; AAG53692.1; -.
DR   PIR; S02270; KIMSCE.
DR   HSSP; P28867; 1PTQ.
DR   MGD; MGI:97599; Prkce.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR002219; DAG_PE-bind.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR000961; Pkinase_C.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   Pfam; PF00130; DAG_PE-bind; 2.
DR   Pfam; PF00168; C2; 1.
DR   Pfam; PF00433; pkinase_C; 1.
DR   PRINTS; PR00008; DAGPEDOMAIN.
DR   ProDom; PD000001; Euk_pkinase; 1.
DR   SMART; SM00109; C1; 2.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00133; S_TK_X; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS50004; C2_DOMAIN_2; 1.
DR   PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR   PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   Repeat; ATP-binding; Transferase; Phosphorylation;
KW   Serine/threonine-protein kinase; Phorbol-ester binding; Zinc.
FT   DOMAIN        1     99       C2 DOMAIN.
FT   DOMAIN      170    220       PHORBOL-ESTER AND DAG BINDING 1.
FT   DOMAIN      243    292       PHORBOL-ESTER AND DAG BINDING 2.
FT   DOMAIN      408    668       PROTEIN KINASE.
FT   NP_BIND     414    422       ATP (BY SIMILARITY).
FT   BINDING     437    437       ATP (BY SIMILARITY).
FT   ACT_SITE    532    532       BY SIMILARITY.
FT   MOD_RES     703    703       PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT   MOD_RES     710    710       PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ   SEQUENCE   737 AA;  83560 MW;  7AEBB8CC10C99F57 CRC64;

  Query Match             100.0%;  Score 48;  DB 1;  Length 737;
  Best Local Similarity   100.0%;  Pred. No. 0.033;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HDAPIGYD 8
           ||||||||
Db      85 HDAPIGYD 92


RESULT 4
KPCE_RAT
ID   KPCE_RAT       STANDARD;      PRT;   737 AA.
AC   P09216;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-MAR-1989 (Rel. 10, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Protein kinase C, epsilon type (EC 2.7.1.-) (nPKC-epsilon).
GN   PRKCE OR PKCE.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=88198270; PubMed=2834397;
RA   Ono Y., Fujii T., Ogita K., Kikkawa U., Igarashi K., Nishizuka Y.;
RT   "The structure, expression, and properties of additional members of
RT   the protein kinase C family.";
RL   J. Biol. Chem. 263:6927-6932(1988).
RN   [2]
RP   SEQUENCE OF 135-297 FROM N.A.
RX   MEDLINE=88083621; PubMed=3691811;
RA   Ono Y., Fujii T., Ogita K., Kikkawa U., Igarashi K., Nishizuka Y.;
RT   "Identification of three additional members of rat protein kinase C
RT   family: delta-, epsilon- and zeta-subspecies.";
RL   FEBS Lett. 226:125-128(1987).
CC   -!- FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-DEPENDENT,
CC       SERINE- AND THREONINE-SPECIFIC ENZYME.
CC   -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC       PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC       THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC   -!- SIMILARITY: CONTAINS 2 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
CC       BINDING DOMAINS.
CC   -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC       PKC SUBFAMILY.
CC   ---------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commerci
CC   entities requires a license agreement (See http://www.isb-sib.ch/announc
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M18331; AAA41872.1; -.
DR   PIR; B28163; KIRTCE.
DR   HSSP; P28867; 1PTQ.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR002219; DAG_PE-bind.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR000961; Pkinase_C.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   Pfam; PF00130; DAG_PE-bind; 2.
DR   Pfam; PF00168; C2; 1.
DR   Pfam; PF00433; pkinase_C; 1.
DR   PRINTS; PR00008; DAGPEDOMAIN.
DR   ProDom; PD000001; Euk_pkinase; 1.
DR   SMART; SM00109; C1; 2.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00133; S_TK_X; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS50004; C2_DOMAIN_2; 1.
DR   PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR   PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.
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DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   Repeat; ATP-binding; Transferase; Phosphorylation;
KW   Serine/threonine-protein kinase; Phorbol-ester binding; Zinc.
FT   DOMAIN        1     99       C2 DOMAIN.
FT   DOMAIN      170    220       PHORBOL-ESTER AND DAG BINDING 1.
FT   DOMAIN      243    292       PHORBOL-ESTER AND DAG BINDING 2.
FT   DOMAIN      408    668       PROTEIN KINASE.
FT   NP_BIND     414    422       ATP (BY SIMILARITY).
FT   BINDING     437    437       ATP (BY SIMILARITY).
FT   ACT_SITE    532    532       BY SIMILARITY.
FT   MOD_RES     703    703       PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT   MOD_RES     710    710       PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ   SEQUENCE   737 AA;  83478 MW;  6AD6999EFDD2659F CRC64;

  Query Match             100.0%;  Score 48;  DB 1;  Length 737;
  Best Local Similarity   100.0%;  Pred. No. 0.033;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 HDAPIGYD 8
           ||||||||
Db      85 HDAPIGYD 92


RESULT 5
KPCL_HUMAN
ID   KPCL_HUMAN     STANDARD;      PRT;   682 AA.
AC   P24723; Q16246;
DT   01-MAR-1992 (Rel. 21, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Protein kinase C, eta type (EC 2.7.1.-) (nPKC-eta) (PKC-L).
GN   PRKCH OR PKCL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=91094824; PubMed=1986216;
RA   Bacher N., Zisman Y., Berent E., Livneh E.;
RT   "Isolation and characterization of PKC-L, a new member of the protein
RT   kinase C-related gene family specifically expressed in lung, skin,
RT   and heart.";
RL   Mol. Cell. Biol. 11:126-133(1991).
RN   [2]
RP   REVISIONS.
RX   MEDLINE=92186874; PubMed=1545821;
RA   Bacher N., Zisman Y., Berent E., Livneh E.;
RL   Mol. Cell. Biol. 12:1404-1404(1992).
RN   [3]
RP   SEQUENCE OF 437-538 FROM N.A.
RX   MEDLINE=95080426; PubMed=7988719;
RA   Palmer R.H., Ridden J., Parker P.J.;
RT   "Identification of multiple, novel, protein kinase C-related gene
RT   products.";
RL   FEBS Lett. 356:5-8(1994).
CC   -!- FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-DEPENDENT,
CC       SERINE- AND THREONINE-SPECIFIC ENZYME.
CC   -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC       PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC       THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC   -!- TISSUE SPECIFICITY: MOST ABUNDANT IN LUNG TISSUE, LESS IN HEART
CC       AND SKIN TISSUE.
CC   -!- SIMILARITY: CONTAINS 2 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
CC       BINDING DOMAINS.
CC   -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC       PKC SUBFAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M55284; AAA60100.1; -.
DR   EMBL; S74620; AAB32724.1; -.
DR   PIR; A39666; A39666.
DR   HSSP; P28867; 1PTQ.
DR   Genew; HGNC:9403; PRKCH.
DR   MIM; 605437; -.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR002219; DAG_PE-bind.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR000961; Pkinase_C.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   Pfam; PF00130; DAG_PE-bind; 2.
DR   Pfam; PF00168; C2; 1.
DR   Pfam; PF00433; pkinase_C; 1.
DR   PRINTS; PR00008; DAGPEDOMAIN.
DR   ProDom; PD000001; Euk_pkinase; 1.
DR   SMART; SM00109; C1; 2.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00133; S_TK_X; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS50004; C2_DOMAIN_2; 1.
DR   PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR   PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   Repeat; ATP-binding; Transferase;
KW   Serine/threonine-protein kinase; Phorbol-ester binding; Zinc.
FT   DOMAIN       12    112       C2 DOMAIN.
FT   DOMAIN      171    221       PHORBOL-ESTER AND DAG BINDING 1.
FT   DOMAIN      245    294       PHORBOL-ESTER AND DAG BINDING 2.
FT   DOMAIN      354    613       PROTEIN KINASE.
FT   NP_BIND     360    368       ATP (BY SIMILARITY).
FT   BINDING     383    383       ATP (BY SIMILARITY).
FT   ACT_SITE    478    478       BY SIMILARITY.
FT   CONFLICT    471    471       D -> E (IN REF. 3).
SQ   SEQUENCE   682 AA;  77563 MW;  13D4EAB01F3B5AB8 CRC64;

  Query Match             79.2%;  Score 38;  DB 1;  Length 682;
  Best Local Similarity   62.5%;  Pred. No. 3.9;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 HDAPIGYD 8
           |: :|:|||
Db      88 HETPLGYD 95


RESULT 6
KPCL_MOUSE
ID   KPCL_MOUSE     STANDARD;      PRT;   683 AA.
AC   P23298;
DT   01-NOV-1991 (Rel. 20, Created)
DT   01-NOV-1991 (Rel. 20, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Protein kinase C, eta type (EC 2.7.1.-) (nPKC-eta) (PKC-L).
GN   PRKCH OR PKCH.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Epidermis;
RX   MEDLINE=91093089; PubMed=2266135;
RA   Osada S.I., Mizuno K., Saido T.C., Akita Y., Suzuki K., Kuroki T.,
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RA   Ohno S.;
RT   "A phorbol ester receptor/protein kinase, nPKC eta, a new member of
RT   the protein kinase C family predominantly expressed in lung and
RT   skin.";
RL   J. Biol. Chem. 265:22434-22440(1990).
CC   -!- FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-DEPENDENT,
CC       SERINE- AND THREONINE-SPECIFIC ENZYME.
CC   -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC       PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC       THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC   -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN LUNK AND SKIN.
CC   -!- SIMILARITY: CONTAINS 2 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
CC       BINDING DOMAINS.
CC   -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC       PKC SUBFAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D90242; BAA14288.1; -.
DR   PIR; A23690; A23690.
DR   HSSP; P28867; 1PTQ.
DR   MGD; MGI:97600; Prkch.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR002219; DAG_PE-bind.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR000961; Pkinase_C.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   Pfam; PF00130; DAG_PE-bind; 2.
DR   Pfam; PF00168; C2; 1.
DR   Pfam; PF00433; pkinase_C; 1.
DR   PRINTS; PR00008; DAGPEDOMAIN.
DR   ProDom; PD000001; Euk_pkinase; 1.
DR   SMART; SM00109; C1; 2.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00133; S_TK_X; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS50004; C2_DOMAIN_2; 1.
DR   PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR   PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Transferase; Serine/threonine-protein kinase;
KW   Phorbol-ester binding; Zinc; Repeat.
FT   DOMAIN       12    102       C2 DOMAIN.
FT   DOMAIN      172    222       PHORBOL-ESTER AND DAG BINDING 1.
FT   DOMAIN      246    295       PHORBOL-ESTER AND DAG BINDING 2.
FT   DOMAIN      355    614       PROTEIN KINASE.
FT   NP_BIND     361    369       ATP (BY SIMILARITY).
FT   BINDING     384    384       ATP (BY SIMILARITY).
FT   ACT_SITE    479    479       BY SIMILARITY.
SQ   SEQUENCE   683 AA;  77973 MW;  C7DB338A9F95F576 CRC64;

  Query Match            79.2%;  Score 38;  DB 1;  Length 683;
  Best Local Similarity  62.5%;  Pred. No. 3.9;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 HDAPIGYD 8
          |: |:|||
Db     88 HETPLGYD 95


RESULT 7
KPCL_RAT
ID   KPCL_RAT       STANDARD;      PRT;   683 AA.
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AC   Q64617;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Protein kinase C, eta type (EC 2.7.1.-) (nPKC-eta) (PKC-L).
GN   PRKCH OR PKCH.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Lung;
RX   MEDLINE=93050193; PubMed=1426252;
RA   Dekker L.V., Parker P.J., McIntyre P.;
RT   "Biochemical properties of rat protein kinase C-eta expressed in COS
RT   cells.";
RL   FEBS Lett. 312:195-199(1992).
CC   -!- FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-DEPENDENT,
CC       SERINE- AND THREONINE-SPECIFIC ENZYME.
CC   -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC       PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC       THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC   -!- SIMILARITY: CONTAINS 2 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
CC       BINDING DOMAINS.
CC   -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC       PKC SUBFAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X68400; CAA48466.1; -.
DR   HSSP; P28867; 1PTQ.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR002219; DAG_PE-bind.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR000961; Pkinase_C.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   Pfam; PF00130; DAG_PE-bind; 2.
DR   Pfam; PF00168; C2; 1.
DR   Pfam; PF00433; pkinase_C; 1.
DR   PRINTS; PR00008; DAGPEDOMAIN.
DR   ProDom; PD000001; Euk_pkinase; 1.
DR   SMART; SM00109; C1; 2.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00133; S_TK_X; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS50004; C2_DOMAIN_2; 1.
DR   PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR   PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Transferase; Serine/threonine-protein kinase;
KW   Phorbol-ester binding; Zinc; Repeat.
FT   DOMAIN       12    102       C2 DOMAIN.
FT   DOMAIN      172    222       PHORBOL-ESTER AND DAG BINDING 1.
FT   DOMAIN      246    295       PHORBOL-ESTER AND DAG BINDING 2.
FT   DOMAIN      355    614       PROTEIN KINASE.
FT   NP_BIND     361    369       ATP (BY SIMILARITY).
FT   BINDING     384    384       ATP (BY SIMILARITY).
FT   ACT_SITE    479    479       BY SIMILARITY.
SQ   SEQUENCE   683 AA;  77946 MW;  2F5B7078D1206510 CRC64;

  Query Match            79.2%;  Score 38;  DB 1;  Length 683;
  Best Local Similarity  62.5%;  Pred. No. 3.9;
```

```
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 HDAPIGYD 8
          |: |:|||
Db     88 HETPLGYD 95


RESULT 8
PO21_NASVI
ID   PO21_NASVI     STANDARD;      PRT;  1025 AA.
AC   Q03278;
DT   01-JUN-1994 (Rel. 29, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Retrovirus-related POL polyprotein from type I retrotransposable
DE   element R2 [Contains: Reverse transcriptase (EC 2.7.7.49);
DE   Endonuclease] (Fragment).
OS   Nasonia vitripennis (Parasitic wasp).
OC   Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC   Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC   Chalcidoidea; Pteromalidae; Nasonia.
OX   NCBI_TaxID=7425;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93196484; PubMed=8383793;
RA   Burke W.D., Eickbush D.G., Xiong Y., Jakubczak J.L., Eickbush T.H.;
RT   "Sequence relationship of retrotransposable elements R1 and R2 within
RT   and between divergent insect species.";
RL   Mol. Biol. Evol. 10:163-185(1993).
RN   [2]
RP   REVISIONS.
RA   Burke W.D., Eickbush D.G., Xiong Y., Jakubczak J.L., Eickbush T.H.;
RL   Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC       + (DNA)(N).
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; L00950; AAC34927.1; -.
DR   PIR; I44490; I44490.
DR   InterPro; IPR000477; RVTse.
DR   InterPro; IPR000822; Znf_C2H2.
DR   Pfam; PF00078; rvt; 1.
DR   Pfam; PF00096; zf-C2H2; 1.
DR   SMART; SM00355; ZnF_C2H2; 1.
DR   PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
DR   PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
KW   Transferase; RNA-directed DNA polymerase; Transposable element;
KW   Hydrolase; Nuclease; Endonuclease; Zinc-finger.
FT   NON_TER       1      1
FT   DOMAIN       <1    754       REVERSE TRANSCRIPTASE.
FT   DOMAIN      755   1025       NUCLEIC ACID-BINDING ENDONUCLEASE.
FT   ZN_FING      46     69       C2H2-TYPE.
SQ   SEQUENCE   1025 AA;  115884 MW;  387BDE63BCF5C518 CRC64;

  Query Match             79.2%;  Score 38;  DB 1;  Length 1025;
  Best Local Similarity   85.7%;  Pred. No. 6;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 HDAPIGY 7
          || ||||
Db    709 HDTPIGY 715


RESULT 9
CCAD_RAT
ID   CCAD_RAT       STANDARD;      PRT;  2203 AA.
AC   P27732; Q63491; Q63492; Q62691; Q01542; O09022; O09023; O09024;
AC   Q62815;
DT   01-OCT-1996 (Rel. 34, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Voltage-dependent L-type calcium channel alpha-1D subunit (Calcium
DE   channel, L type, alpha-1 polypeptide, isoform 2) (RAT brain class D)
DE   (RBD).
GN   CACNA1D OR CACNL1A2 OR CCHL1A2 OR CACH3 OR CACN4.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS CACN4A AND CACN4B).
RC   TISSUE=Insulinoma;
RX   MEDLINE=95280950; PubMed=7760845;
RA   Ihara Y., Yamada Y., Fujii Y., Gonoi T., Yano H., Yasuda K.,
RA   Inagaki N., Seino Y., Seino S.;
RT   "Molecular diversity and functional characterization of voltage-
RT   dependent calcium channels (CACN4) expressed in pancreatic beta-
RT   cells.";
RL   Mol. Endocrinol. 9:121-130(1995).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS TRUNCATED; RB9; RB11; RB34 AND RB48).
RC   TISSUE=Brain;
RX   MEDLINE=91299338; PubMed=1648940;
RA   Hui A., Ellinor P.T., Krizanova O., Wang J.-J., Diebold R.J.,
RA   Schwartz A.;
RT   "Molecular cloning of multiple subtypes of a novel rat brain isoform
RT   of the alpha-1 subunit of the voltage-dependent calcium channel.";
RL   Neuron 7:35-44(1991).
RN   [3]
RP   SEQUENCE OF 1-125 FROM N.A.
RX   MEDLINE=96040125; PubMed=7553731;
RA   Kamp T.J., Mitas M., Fields K.L., Asoh S., Chin H., Marban E.,
RA   Nirenberg M.;
RT   "Transcriptional regulation of the neuronal L-type calcium channel
RT   alpha 1D subunit gene.";
RL   Cell. Mol. Neurobiol. 15:307-326(1995).
RN   [4]
RP   SEQUENCE OF 1100-1410 FROM N.A. (ISOFORMS RKC5 AND RKC6).
RC   TISSUE=Kidney;
RX   MEDLINE=93066265; PubMed=1279681;
RA   Yu A.S.L., Hebert S.C., Brenner B.M., Lytton J.;
RT   "Molecular characterization and nephron distribution of a family of
RT   transcripts encoding the pore-forming subunit of Ca2+ channels in the
RT   kidney.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:10494-10498(1992).
RN   [5]
RP   SEQUENCE OF 1218-1498 FROM N.A. (ISOFORM ROB3).
RC   TISSUE=Osteosarcoma;
RX   MEDLINE=96074617; PubMed=7479909;
RA   Barry E.L.R., Gesek F.A., Froehner S.C., Friedman P.A.;
RT   "Multiple calcium channel transcripts in rat osteosarcoma cells:
RT   selective activation of alpha 1D isoform by parathyroid hormone.";
RL   Proc. Natl. Acad. Sci. U.S.A. 92:10914-10918(1995).
RN   [6]
RP   SEQUENCE OF 1200-1493 FROM N.A. (ISOFORMS RH1; RH2; CACH3A/B AND
RP   DELTA-IVS3/S4).
RC   TISSUE=Hepatoma;
RX   MEDLINE=97376179; PubMed=9232351;
RA   Brereton H.M., Harland M.L., Froscio M., Petronijevic T.,
RA   Barritt G.J.;
RT   "Novel variants of voltage-operated calcium channel alpha-1 subunit
RT   transcripts in a rat liver-derived cell line: deletion in the IVS4
RT   voltage sensing region.";
RL   Cell Calcium 22:39-52(1997).
RN   [7]
RP   SEQUENCE OF 1307-1479 FROM N.A. (ISOFORM RBD-55).
RX   MEDLINE=90239020; PubMed=1692134;
RA   Snutch T.P., Leonard J.P., Gilbert M.M., Lester H.A., Davidson N.;
RT   "Rat brain expresses a heterogeneous family of calcium channels.";
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RL   Proc. Natl. Acad. Sci. U.S.A. 87:3391-3395(1990).
CC   -!- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIATE THE
CC       ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED
CC       IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE
CC       CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,
CC       CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1D
CC       GIVES RISE TO L-TYPE CALCIUM CURRENTS. LONG-LASTING (L-TYPE)
CC       CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA)
CC       GROUP. THEY ARE BLOCKED BY DIHYDROPYRIDINES (DHP),
CC       PHENYLALKYLAMINES, BENZOTHIAZEPINES, AND BY OMEGA-AGATOXIN-IIIA
CC       (OMEGA-AGA-IIIA). THEY ARE HOWEVER INSENSITIVE TO OMEGA-CONOTOXIN-
CC       GVIA (OMEGA-CTX-GVIA) AND OMEGA-AGATOXIN-IVA (OMEGA-AGA-IVA).
CC   -!- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT
CC       COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS
CC       IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-
CC       FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS
CC       SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM
CC       CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA
CC       LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- ALTERNATIVE PRODUCTS: 14 isoforms; CACN4A (shown here), CACN4B,
CC       CACH3A/RB48/RBD-55, Delta-IV-S3, Delta-IV-S4, RB9, RB11, RB34 RH1,
CC       RH2, RKC5, RKC6, ROB3 and a truncated isoform; are produced by
CC       alternative splicing. The region sequenced in isoforms ROB3 and
CC       RKC5 is identical to CACN4.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, PANCREATIC ISLETS AND B-
CC       LYMPHOCYTES.
CC   -!- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE
CC       HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE
CC       POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS
CC       PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
CC       SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
CC   -!- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
CC       FAMILY.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D38101; BAA07282.1; -.
DR   EMBL; D38102; BAA07283.1; -.
DR   EMBL; M57682; AAA42015.1; -.
DR   EMBL; U14005; AAB60515.1; -.
DR   EMBL; M99221; AAA40895.1; -.
DR   EMBL; U31772; AAA89156.1; -.
DR   EMBL; U49126; AAB61634.1; -.
DR   EMBL; U49127; AAB61635.1; -.
DR   EMBL; U49128; AAB61636.1; -.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002077; Ca_channel.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR003091; K_channel.
DR   InterPro; IPR000636; M+channel_nlg.
DR   Pfam; PF00520; ion_trans; 4.
DR   PRINTS; PR00167; CACHANNEL.
DR   PRINTS; PR00169; KCHANNEL.
KW   Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW   Calcium channel; Glycoprotein; Repeat; Multigene family;
KW   Calcium-binding; Phosphorylation; Alternative splicing.
FT   REPEAT      112    408       I.
FT   REPEAT      528    774       II.
FT   REPEAT      892   1174       III.
FT   REPEAT     1211   1486       IV.
FT   DOMAIN        1    126       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    127    145       S1 OF REPEAT I (POTENTIAL).
FT   DOMAIN      146    163       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    164    183       S2 OF REPEAT I (POTENTIAL).
FT   DOMAIN      184    195       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    196    214       S3 OF REPEAT I (POTENTIAL).
FT   DOMAIN      215    235       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    236    254       S4 OF REPEAT I (POTENTIAL).
FT   DOMAIN      255    273       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    274    293       S5 OF REPEAT I (POTENTIAL).
FT   DOMAIN      294    381       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    382    406       S6 OF REPEAT I (POTENTIAL).
FT   DOMAIN      407    582       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    583    602       S1 OF REPEAT II (POTENTIAL).
FT   DOMAIN      603    617       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    618    636       S2 OF REPEAT II (POTENTIAL).
FT   DOMAIN      637    644       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    645    663       S3 OF REPEAT II (POTENTIAL).
FT   DOMAIN      664    673       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    674    692       S4 OF REPEAT II (POTENTIAL).
FT   DOMAIN      693    711       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    712    732       S5 OF REPEAT II (POTENTIAL).
FT   DOMAIN      733    786       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    787    811       S6 OF REPEAT II (POTENTIAL).
FT   DOMAIN      812    945       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    946    964       S1 OF REPEAT III (POTENTIAL).
FT   DOMAIN      965    980       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    981   1000       S2 OF REPEAT III (POTENTIAL).
FT   DOMAIN     1001   1012       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   1013   1031       S3 OF REPEAT III (POTENTIAL).
FT   DOMAIN     1032   1037       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   1038   1057       S4 OF REPEAT III (POTENTIAL).
FT   DOMAIN     1058   1076       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   1077   1096       S5 OF REPEAT III (POTENTIAL).
FT   DOMAIN     1097   1186       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   1187   1207       S6 OF REPEAT III (POTENTIAL).
FT   DOMAIN     1208   1264       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   1265   1283       S1 OF REPEAT IV (POTENTIAL).
FT   DOMAIN     1284   1298       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   1299   1318       S2 OF REPEAT IV (POTENTIAL).
FT   DOMAIN     1319   1325       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   1326   1347       S3 OF REPEAT IV (POTENTIAL).
FT   DOMAIN     1348   1357       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   1358   1377       S4 OF REPEAT IV (POTENTIAL).
FT   DOMAIN     1378   1396       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   1397   1416       S5 OF REPEAT IV (POTENTIAL).
FT   DOMAIN     1417   1483       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   1484   1508       S6 OF REPEAT IV (POTENTIAL).
FT   DOMAIN     1509   2203       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN        1      7       POLY-MET.
FT   DOMAIN      712    718       POLY-LEU.
FT   DOMAIN      886    897       POLY-GLU.
FT   DOMAIN      429    446       BINDING TO THE BETA SUBUNIT (BY
FT                                SIMILARITY).
FT   SITE        364    364       CALCIUM ION SELECTIVITY AND PERMEABILITY
FT                                (BY SIMILARITY).
FT   SITE        763    763       CALCIUM ION SELECTIVITY AND PERMEABILITY
FT                                (BY SIMILARITY).
FT   SITE       1160   1160       CALCIUM ION SELECTIVITY AND PERMEABILITY

  Query Match          77.1%;  Score 37;  DB 1;  Length 2203;
  Best Local Similarity  85.7%;  Pred. No. 23;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 DAPIGYD 8
           |:|||||
Db    1937 DSPIGYD 1943


RESULT 10
FKB5_MOUSE
ID   FKB5_MOUSE     STANDARD;      PRT;   456 AA.
AC   Q64378;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   51 kDa FK506-binding protein (FKBP51) (Peptidyl-prolyl cis-trans
DE   isomerase) (EC 5.2.1.8) (PPiase) (Rotamase).
GN   FKBP5 OR FKBP51.
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OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96074651; PubMed=7479941;
RA   Yeh W.-C., Li T.-K., Bierer B.E., McKnight S.L.;
RT   "Identification and characterization of an immunophilin expressed
RT   during the clonal expansion phase of adipocyte differentiation.";
RL   Proc. Natl. Acad. Sci. U.S.A. 92:11081-11085(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Thymus;
RX   MEDLINE=95349606; PubMed=7542743;
RA   Baughman G., Wiederrecht G.J., Campbell N.F., Martin M.M.,
RA   Bourgeois S.;
RT   "FKBP51, a novel T-cell-specific immunophilin capable of calcineurin
RT   inhibition.";
RL   Mol. Cell. Biol. 15:4395-4402(1995).
CC   -!- FUNCTION: INTERACTS WITH PROGESTERONE RECEPTOR (BY SIMILARITY).
CC   -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC       PEPTIDE BONDS IN OLIGOPEPTIDES.
CC   -!- ENZYME REGULATION: INHIBITED BY BOTH FK506 AND RAPAMYCIN.
CC   -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
CC   -!- TISSUE SPECIFICITY: WIDELY EXPRESSED, HIGHEST LEVELS FOUND IN THE
CC       LIVER, SKELETAL MUSCLE, KIDNEY AND THYMUS. EXPRESSION IS REGULATED
CC       DURING ADIPOCYTE DIFFERENTIATION.
CC   -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY. CONTAINS 2
CC       FKBP-LIKE DOMAINS.
CC   -!- SIMILARITY: CONTAINS 3 TPR REPEATS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U36220; AAA89162.1; -.
DR   EMBL; U16959; AAA86983.1; -.
DR   HSSP; P27124; 1ROT.
DR   MGD; MGI:104670; Fkbp5.
DR   InterPro; IPR001179; FKBP_PPIase.
DR   InterPro; IPR001440; TPR.
DR   Pfam; PF00254; FKBP; 2.
DR   Pfam; PF00515; TPR; 2.
DR   PROSITE; PS00453; FKBP_PPIASE_1; 1.
DR   PROSITE; PS00454; FKBP_PPIASE_2; 1.
DR   PROSITE; PS50059; FKBP_PPIASE_3; 2.
KW   Isomerase; Rotamase; TPR repeat; Repeat; Nuclear protein.
FT   DOMAIN       50    138       PPIASE, FKBP-TYPE 1.
FT   DOMAIN      165    251       PPIASE, FKBP-TYPE 2.
FT   REPEAT      268    301       TPR 1.
FT   REPEAT      317    350       TPR 2.
FT   REPEAT      352    384       TPR 3.
SQ   SEQUENCE   456 AA;  50966 MW;  8FD0C9B61478EB46 CRC64;

  Query Match             72.9%;  Score 35;  DB 1;  Length 456;
  Best Local Similarity   75.0%;  Pred. No. 11;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 HDAPIGYD 8
            || ||| |
Db     196 HDIPIGID 203


RESULT 11
FKB5_HUMAN
ID   FKB5_HUMAN     STANDARD;      PRT;   457 AA.
AC   Q13451;
DT   01-NOV-1997 (Rel. 35, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   51 kDa FK506-binding protein (FKBP51) (Peptidyl-prolyl cis-trans
DE   isomerase) (EC 5.2.1.8) (PPIase) (Rotamase) (54 kDa progesterone
DE   receptor-associated immunophilin) (FKBP54) (P54) (FF1 antigen)
DE   (HSP90-binding immunophilin) (Androgen-regulated protein 6).
GN   FKBP5 OR AIG6.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Thymus;
RX   MEDLINE=97242207; PubMed=9125197;
RA   Baughman G., Wiederrecht G.J., Chang F., Martin M.M., Bourgeois S.;
RT   "Tissue distribution and abundance of human FKBP51, an FK506-binding
RT   protein that can mediate calcineurin inhibition.";
RL   Biochem. Biophys. Res. Commun. 232:437-443(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Zhang J.S., Smith D.I.;
RT   "Identification of AIG6 as an androgen response gene in human prostate
RT   cancer cell line LNCaP.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE OF 9-457 FROM N.A.
RX   MEDLINE=97154494; PubMed=9001212;
RA   Nair S.C., Rimerman R.A., Toran E.J., Chen S., Prapapanich V.,
RA   Butts R.N., Smith D.F.;
RT   "Molecular cloning of human FKBP51 and comparisons of immunophilin
RT   interactions with Hsp90 and progesterone receptor.";
RL   Mol. Cell. Biol. 17:594-603(1997).
RN   [4]
RP   CHARACTERIZATION.
RX   MEDLINE=94043261; PubMed=7693698;
RA   Smith D.F., Albers M.W., Schreiber S.L., Leach K.L., Deibel M.R. Jr.;
RT   "FKBP54, a novel FK506-binding protein in avian progesterone receptor
RT   complexes and HeLa extracts.";
RL   J. Biol. Chem. 268:24270-24273(1993).
CC   -!- FUNCTION: INTERACTS WITH FUNCTIONALLY MATURE HETERO-OLIGOMERIC
CC       PROGESTERONE RECEPTOR COMPLEXES ALONG WITH HSP90 AND P23.
CC   -!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC       PEPTIDE BONDS IN OLIGOPEPTIDES.
CC   -!- ENZYME REGULATION: INHIBITED BY FK506 BUT NOT CYCLOSPORIN.
CC   -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
CC   -!- TISSUE SPECIFICITY: WIDELY EXPRESSED, ENRICHED IN TESTIS COMPARED
CC       TO OTHER TISSUES.
CC   -!- INDUCTION: By androgen.
CC   -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY. CONTAINS 2
CC       FKBP-LIKE DOMAINS.
CC   -!- SIMILARITY: CONTAINS 3 TPR REPEATS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U71321; AAC51189.1; -.
DR   EMBL; AF194172; AAL54872.1; -.
DR   EMBL; U42031; AAA86245.1; -.
DR   HSSP; P27124; 1ROT.
DR   Genew; HGNC:3721; FKBP5.
DR   MIM; 602623; -.
DR   InterPro; IPR001179; FKBP_PPIase.
DR   InterPro; IPR001440; TPR.
DR   Pfam; PF00254; FKBP; 2.
DR   Pfam; PF00515; TPR; 2.
DR   PROSITE; PS00453; FKBP_PPIASE_1; 1.
DR   PROSITE; PS00454; FKBP_PPIASE_2; 1.
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DR   PROSITE; PS50059; FKBP_PPIASE_3; 2.
KW   Isomerase; Rotamase; TPR repeat; Repeat; Nuclear protein.
FT   DOMAIN       42    130       PPIASE, FKBP-TYPE 1.
FT   DOMAIN      157    243       PPIASE, FKBP-TYPE 2.
FT   REPEAT      268    301       TPR 1.
FT   REPEAT      317    350       TPR 2.
FT   REPEAT      352    384       TPR 3.
SQ   SEQUENCE   457 AA;  51212 MW;  18A86608C6891A73 CRC64;

  Query Match             72.9%;  Score 35;  DB 1;  Length 457;
  Best Local Similarity   75.0%;  Pred. No. 11;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 HDAPIGYD 8
           || ||| |
Db     196 HDIPIGID 203


RESULT 12
VATB_HALVO
ID   VATB_HALVO     STANDARD;      PRT;   468 AA.
AC   Q48333;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   V-type ATP synthase beta chain (EC 3.6.3.14) (V-type ATPase subunit
DE   B).
GN   ATPB.
OS   Halobacterium volcanii (Haloferax volcanii).
OC   Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC   Halobacteriaceae; Haloferax.
OX   NCBI_TaxID=2246;
RN   [1]
RP   SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC   STRAIN=WR 340;
RX   MEDLINE=95322432; PubMed=7599166;
RA   Steinert K., Kroth-Pancic P.G., Bickel-Sandkoetter S.;
RT   "Nucleotide sequence of the ATPase A- and B-subunits of the
RT   halophilic archaebacterium Haloferax volcanii and characterization of
RT   the enzyme.";
RL   Biochim. Biophys. Acta 1249:137-144(1995).
CC   -!- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
CC       GRADIENT ACROSS THE MEMBRANE. THE ARCHAEAL BETA CHAIN IS A
CC       REGULATORY SUBUNIT.
CC   -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
CC       H(+)(Out).
CC   -!- SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X79516; CAA56052.1; -.
DR   InterPro; IPR000793; ATPase_a/bC.
DR   InterPro; IPR004100; ATPase_a/bN.
DR   InterPro; IPR000194; ATPase_a/bcentre.
DR   Pfam; PF00006; ATP-synt_ab; 1.
DR   Pfam; PF00306; ATP-synt_ab_C; 1.
DR   Pfam; PF02874; ATP-synt_ab_N; 1.
DR   TIGRFAMs; TIGR01041; ATP_syn_B_arch; 1.
DR   PROSITE; PS00152; ATPASE_ALPHA_BETA; 1.
KW   Hydrolase; ATP synthesis; Hydrogen ion transport.
SQ   SEQUENCE   468 AA;  52018 MW;  B97D059AEF6071BB CRC64;

  Query Match             72.9%;  Score 35;  DB 1;  Length 468;
  Best Local Similarity   85.7%;  Pred. No. 11;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 DAPIGYD 8
           | |||||
Db      20 DEPIGYD 26


RESULT 13
VATB_HALN1
ID   VATB_HALN1     STANDARD;      PRT;   471 AA.
AC   Q9HNE4;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   V-type ATP synthase beta chain (EC 3.6.3.14) (V-type ATPase subunit
DE   B).
GN   ATPB OR VNG2138G.
OS   Halobacterium sp. (strain NRC-1).
OC   Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC   Halobacteriaceae; Halobacterium.
OX   NCBI_TaxID=64091;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20504483; PubMed=11016950;
RA   Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA   Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
RA   Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA   Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA   Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA   Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA   Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA   Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
RT   "Genome sequence of Halobacterium species NRC-1.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
CC   -!- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
CC       GRADIENT ACROSS THE MEMBRANE. THE ARCHAEAL BETA CHAIN IS A
CC       REGULATORY SUBUNIT.
CC   -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
CC       H(+)(Out).
CC   -!- SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AE005102; AAG20276.1; -.
DR   InterPro; IPR000793; ATPase_a/bC.
DR   InterPro; IPR004100; ATPase_a/bN.
DR   InterPro; IPR000194; ATPase_a/bcentre.
DR   Pfam; PF00006; ATP-synt_ab; 1.
DR   Pfam; PF00306; ATP-synt_ab_C; 1.
DR   Pfam; PF02874; ATP-synt_ab_N; 1.
DR   TIGRFAMs; TIGR01041; ATP_syn_B_arch; 1.
DR   PROSITE; PS00152; ATPASE_ALPHA_BETA; 1.
KW   Hydrolase; ATP synthesis; Hydrogen ion transport; Complete proteome.
SQ   SEQUENCE   471 AA;  51957 MW;  12DB1835E0EA9E62 CRC64;

  Query Match             72.9%;  Score 35;  DB 1;  Length 471;
  Best Local Similarity   85.7%;  Pred. No. 11;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 DAPIGYD 8
           | |||||
Db      20 DEPIGYD 26


RESULT 14
VATB_HALSA
ID   VATB_HALSA     STANDARD;      PRT;   471 AA.
AC   P25164;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
```

```
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   V-type ATP synthase beta chain (EC 3.6.3.14) (V-type ATPase subunit
DE   B).
GN   ATPB.
OS   Halobacterium salinarium.
OC   Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC   Halobacteriaceae; Halobacterium.
OX   NCBI_TaxID=2242;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 1-8; 272-344; 425-444 AND 446-471.
RX   MEDLINE=91378275; PubMed=1832829;
RA   Ihara K., Mukohata Y.;
RT   "The ATP synthase of Halobacterium salinarium (halobium) is an
RT   archaebacterial type as revealed from the amino acid sequences of its
RT   two major subunits.";
RL   Arch. Biochem. Biophys. 286:111-116(1991).
CC   -!- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
CC       GRADIENT ACROSS THE MEMBRANE. THE ARCHAEAL BETA CHAIN IS A
CC       REGULATORY SUBUNIT.
CC   -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
CC       H(+)(Out).
CC   -!- SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X70294; CAA49776.1; -.
DR   PIR; S14733; S14733.
DR   InterPro; IPR000793; ATPase_a/bC.
DR   InterPro; IPR004100; ATPase_a/bN.
DR   InterPro; IPR000194; ATPase_a/bcentre.
DR   Pfam; PF00006; ATP-synt_ab; 1.
DR   Pfam; PF00306; ATP-synt_ab_C; 1.
DR   Pfam; PF02874; ATP-synt_ab_N; 1.
DR   TIGRFAMs; TIGR01041; ATP_syn_B_arch; 1.
DR   PROSITE; PS00152; ATPASE_ALPHA_BETA; 1.
KW   Hydrolase; ATP synthesis; Hydrogen ion transport.
SQ   SEQUENCE   471 AA;  51956 MW;  749A55F7B5B34823 CRC64;

  Query Match             72.9%;  Score 35;  DB 1;  Length 471;
  Best Local Similarity   85.7%;  Pred. No. 11;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 DAPIGYD 8
           | |||||
Db      20 DEPIGYD 26


RESULT 15
CHI1_BACCI
ID   CHI1_BACCI     STANDARD;      PRT;   699 AA.
AC   P20533;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   01-FEB-1995 (Rel. 31, Last annotation update)
DE   Chitinase A1 precursor (EC 3.2.1.14).
GN   CHIA1.
OS   Bacillus circulans.
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=1397;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=WL-12;
RX   MEDLINE=90368776; PubMed=2203782;
RA   Watanabe T., Suzuki K., Oyanagi W., Ohnishi K., Tanaka H.;
RT   "Gene cloning of chitinase A1 from Bacillus circulans WL-12 revealed
RT   its evolutionary relationship to Serratia chitinase and to the type
RT   III homology units of fibronectin.";
RL   J. Biol. Chem. 265:15659-15665(1990).
RN   [2]
RP   MUTAGENESIS.
RC   STRAIN=WL-12;
RX   MEDLINE=93366760; PubMed=8103047;
RA   Watanabe T., Kohori K., Miyashita K., Fujii T., Sakai H.,
RA   Uchida M., Tanaka H.;
RT   "Identification of glutamic acid 204 and aspartic acid 200 in
RT   chitinase A1 of Bacillus circulans WL-12 as essential residues for
RT   chitinase activity.";
RL   J. Biol. Chem. 268:18567-18572(1993).
CC   -!- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-
CC       acetyl-D-glucosamine polymers of chitin.
CC   -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC   -!- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL
CC       HYDROLASES).
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M57601; AAA81528.1; -.
DR   PIR; A38368; A38368.
DR   HSSP; P02751; 1FNA.
DR   InterPro; IPR003610; CBM_5_12.
DR   InterPro; IPR001579; Chitinase_18/2.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003962; FnIII_repeat.
DR   InterPro; IPR001223; Glyco_hydro_18.
DR   Pfam; PF00041; fn3; 2.
DR   Pfam; PF00704; Glyco_hydro_18; 1.
DR   Pfam; PF02839; CBM_5_12; 1.
DR   PRINTS; PR00014; FNTYPEIII.
DR   ProDom; PD000471; Glyco_hydro_18; 2.
DR   SMART; SM00495; ChtBD3; 1.
DR   SMART; SM00060; FN3; 2.
DR   PROSITE; PS01095; CHITINASE_18; 1.
KW   Hydrolase; Glycosidase; Chitin degradation; Signal; Repeat.
FT   SIGNAL        1     41
FT   CHAIN        42    699       CHITINASE A1.
FT   DOMAIN       42    460       CATALYTIC.
FT   DOMAIN      465    549       FIBRONECTIN TYPE-III (R-1).
FT   DOMAIN      560    644       FIBRONECTIN TYPE-III (R-2).
FT   ACT_SITE    204    204       PROTON DONOR (PROBABLE).
FT   MUTAGEN     200    200       D->N: DECREASE IN ACTIVITY.
FT   MUTAGEN     200    200       D->E: NO CHANGE IN ACTIVITY.
FT   MUTAGEN     204    204       E->D,Q: LOSS OF ACTIVITY.
SQ   SEQUENCE   699 AA;  73677 MW;  AC7C9B22E2987643 CRC64;

  Query Match             72.9%;  Score 35;  DB 1;  Length 699;
  Best Local Similarity   62.5%;  Pred. No. 17;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 HDAPIGYD 8
           |:||: ||
Db     291 HNAPLNYD 298


Search completed: March 14, 2003, 09:21:17
Job time : 14 secs
```

GenCore version 5.1.4_p5_4578

OM protein - protein search, using sw model

Run on: March 14, 2003, 09:20:39 ; Search time 29 Seconds
(without alignments)
56.841 Million cell updates/sec

Title: US-10-007-363-2
Perfect score: 48
Sequence: 1 HDAPIGYD 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	39	81.2	652	3	O60070	O60070 schizosacch
2	39	81.2	869	13	O42126	O42126 xenopus lae
3	37	77.1	493	5	O44320	O44320 hippodamia
4	37	77.1	695	11	Q91WX8	Q91wx8 rattus norv
5	35	72.9	171	2	Q9F5F3	Q9f5f3 agrobacteri
6	35	72.9	180	10	Q9LZG9	Q9lzg9 arabidopsis
7	35	72.9	199	2	Q9R6J9	Q9r6j9 agrobacteri
8	35	72.9	199	16	Q8U626	Q8u626 agrobacteri
9	35	72.9	218	16	Q8XHB1	Q8xhb1 clostridium
10	35	72.9	371	5	Q9NAM5	Q9nam5 caenorhabdi
11	35	72.9	437	3	O74958	O74958 schizosacch
12	35	72.9	457	6	Q9XSH5	Q9xsh5 saimiri bol
13	35	72.9	457	6	Q9XT11	Q9xt11 aotus nancy
14	35	72.9	457	6	Q9XSI2	Q9xsi2 saguinus oe
15	35	72.9	457	6	Q95L05	Q95l05 cercopithec
16	34.5	71.9	553	10	O49931	O49931 pisum sativ
17	34	70.8	177	2	Q9EUW4	Q9euw4 listeria in
18	34	70.8	205	16	Q9ZLM9	Q9zlm9 helicobacte
19	34	70.8	245	2	Q93H02	Q93h02 streptomyce
20	34	70.8	285	3	Q9P3S0	Q9p3s0 neurospora
21	34	70.8	304	12	O39253	O39253 equine herp
22	34	70.8	323	2	Q9AG01	Q9ag01 shigella fl
23	34	70.8	326	5	Q18648	Q18648 caenorhabdi
24	34	70.8	335	5	Q9W2V4	Q9w2v4 drosophila
25	34	70.8	387	5	Q9VZX1	Q9vzx1 drosophila
26	34	70.8	392	16	Q8YLF2	Q8ylf2 anabaena sp
27	34	70.8	401	2	Q47476	Q47476 escherichia
28	34	70.8	411	16	Q97L71	Q97l71 clostridium
29	34	70.8	424	2	Q8VSQ3	Q8vsq3 shigella fl
30	34	70.8	458	5	Q9VF23	Q9vf23 drosophila
31	34	70.8	463	10	Q9AU48	Q9au48 dioscorea e
32	34	70.8	470	2	Q99QR0	Q99qr0 shigella fl
33	34	70.8	470	2	Q8VSJ7	Q8vsj7 shigella fl
34	34	70.8	483	16	Q8ZAN2	Q8zan2 yersinia pe
35	34	70.8	484	2	Q99QI8	Q99qi8 shigella fl
36	34	70.8	484	2	Q99QF4	Q99qf4 shigella fl
37	34	70.8	484	2	Q8VSL8	Q8vsl8 shigella fl
38	34	70.8	484	2	Q8VSI5	Q8vsi5 shigella fl
39	34	70.8	550	5	Q8SQW5	Q8sqw5 encephalito
40	34	70.8	596	10	Q94I35	Q94i35 oryza sativ
41	34	70.8	668	17	Q8TX28	Q8tx28 methanopyru
42	34	70.8	675	16	Q8ZG01	Q8zg01 yersinia pe
43	34	70.8	677	16	Q9HYC7	Q9hyc7 pseudomonas
44	34	70.8	677	16	Q8ZNN4	Q8znn4 salmonella
45	34	70.8	677	16	Q8Z5C3	Q8z5c3 salmonella

ALIGNMENTS

RESULT 1
O60070
ID O60070 PRELIMINARY; PRT; 652 AA.
AC O60070;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 74.3 kDa protein C13G1.08C in chromosome II.
GN SPBC13G1.08C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Lyne M., Wood V., Rajandream M.A., Barrell B.G., Badcock K.,
RA Churcher C.M.;
RL Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: SOME, TO HUMAN ASH2L.
DR EMBL; AL022600; CAA18661.1; -.
DR InterPro; IPR003878; SPRY_domain.
DR InterPro; IPR003877; SPRY_receptor.
DR InterPro; IPR001965; Znf_PHD.
DR Pfam; PF00622; SPRY; 1.
DR SMART; SM00249; PHD; 1.
DR SMART; SM00449; SPRY; 1.
KW Hypothetical protein.
SQ SEQUENCE 652 AA; 74252 MW; 998E783EC8BD0360 CRC64;

Query Match 81.2%; Score 39; DB 3; Length 652;
Best Local Similarity 85.7%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DAPIGYD 8
|||:|||
Db 419 DAPVGYD 425

```
RESULT 2
O42126
ID   O42126      PRELIMINARY;      PRT;   869 AA.
AC   O42126;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Vitellogenin receptor.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=OOCYTE;
RA   Okabayashi K.;
RL   Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=OOCYTE;
RX   MEDLINE=96295501; PubMed=8702402;
RA   Okabayashi K., Shoji H., Nakamura T., Hashimoto O., Asashima M.,
RA   Sugino H.;
RT   "cDNA Cloning and Expression of the Xenopus laevis Vitellogenin
RT   Receptor.";
RL   Biochem. Biophys. Res. Commun. 224:406-413(1996).
DR   EMBL; AB006906; BAA22145.1; -.
DR   HSSP; P01130; 1AJJ.
DR   InterPro; IPR000152; Asx_hydroxyl.
DR   InterPro; IPR000561; EGF-like.
DR   InterPro; IPR001881; EGF_Ca.
DR   InterPro; IPR000033; Ldl_receptor_rep.
DR   InterPro; IPR002172; LDL_recept_A.
DR   Pfam; PF00057; ldl_recept_a; 8.
DR   Pfam; PF00058; ldl_recept_b; 5.
DR   PRINTS; PR00261; LDLRECEPTOR.
DR   SMART; SM00179; EGF_CA; 1.
DR   SMART; SM00001; EGF_like; 2.
DR   SMART; SM00192; LDLa; 8.
DR   SMART; SM00135; LY; 5.
DR   PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_2.
DR   PROSITE; PS01186; EGF_2; 3.
DR   PROSITE; PS01187; EGF_CA; 2.
DR   PROSITE; PS01209; LDLRA_1; 8.
DR   PROSITE; PS50068; LDLRA_2; 8.
KW   Calcium-binding; EGF-like domain; Glycoprotein; Receptor; Repeat.
SQ   SEQUENCE   869 AA;  96378 MW;  A57A3B34072EB517 CRC64;

  Query Match             81.2%;  Score 39;  DB 13;  Length 869;
  Best Local Similarity   75.0%;  Pred. No. 42;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 HDAPIGYD 8
           || ||||:
Db     371 HDLPIGYE 378


RESULT 3
O44320
ID   O44320      PRELIMINARY;      PRT;   493 AA.
AC   O44320;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Reverse transcriptase (Fragment).
GN   R2 ORF.
OS   Hippodamia convergens (Convergent lady beetle).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC   Cucujiformia; Coccinellidae; Coccinellinae; Hippodamia.
OX   NCBI_TaxID=64696;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Burke W.D., Malik H.S., Eickbush T.H.;
RT   "R1 and R2 Provide an Estimate of the Age and Stability of
RT   Retrotransposons.";
RL   Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF015816; AAB94040.1; -.
DR   InterPro; IPR000477; RVTse.
DR   Pfam; PF00078; rvt; 1.
KW   RNA-directed DNA polymerase.
FT   NON_TER       1       1
SQ   SEQUENCE   493 AA;  55882 MW;  9F776B92C636B9C9 CRC64;

  Query Match             77.1%;  Score 37;  DB 5;  Length 493;
  Best Local Similarity   71.4%;  Pred. No. 56;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 HDAPIGY 7
           || |:||
Db     159 HDVPVGY 165


RESULT 4
Q91WX8
ID   Q91WX8      PRELIMINARY;      PRT;   695 AA.
AC   Q91WX8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Voltage-gated calcium channel pore forming subunit CaV1.3alpha1
DE   (Fragment).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=SUPERIOR CERVICAL GANGLIA;
RX   MEDLINE=21380268; PubMed=11487617;
RA   Xu W., Lipscombe D.;
RT   "Neuronal Ca(V)1.3alpha(1) L-type channels activate at relatively
RT   hyperpolarized membrane potentials and are incompletely inhibited by
RT   dihydropyridines.";
RL   J. Neurosci. 21:5944-5951(2001).
DR   EMBL; AF370010; AAK72960.1; -.
FT   NON_TER       1       1
SQ   SEQUENCE   695 AA;  79034 MW;  B9A5A1CE11FB7D32 CRC64;

  Query Match             77.1%;  Score 37;  DB 11;  Length 695;
  Best Local Similarity   85.7%;  Pred. No. 82;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2 DAPIGYD 8
           |:|||||
Db     429 DSPIGYD 435


RESULT 5
Q9F5F3
ID   Q9F5F3      PRELIMINARY;      PRT;   171 AA.
AC   Q9F5F3;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   Riorf97 protein.
GN   RIORF97.
OS   Agrobacterium rhizogenes.
OG   Plasmid pRi1724.
OC   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC   Rhizobiaceae; Rhizobium.
OX   NCBI_TaxID=359;
RN   [1]
RP   SEQUENCE FROM N.A.
```

```
RC   STRAIN=MAFF03-01724;
RA   Moriguchi K., Maeda Y., Satou M., Satuti N., Kataoka M., Tanaka N.,
RA   Yoshida K.;
RT   "The complete nucleotide sequence of a Ri (root inducing) plasmid
RT   indicates its chimerical structure between Ti and Sym plasmids.";
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MAFF03-01724;
RA   Moriguchi K., Maeda Y., Satou M., Kataoka M., Tanaka N., Yoshida K.;
RT   "Analysis of unique variable region of a plant root inducing plasmid,
RT   pRi1724, by the construction of its physical map and library.";
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MAFF03-01724;
RA   Moriguchi K., Nishida T., Maeda Y., Tanaka N., Yoshida K.;
RT   "Genome structure of Ri plasmid (1):Construction of linking library
RT   and physical map of pRi1724 in Japanese Agrobacterium.";
RL   Nucleic Acids Symp. Ser. 39:189-190(1998).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MAFF03-01724;
RX   MEDLINE=20241294; PubMed=10780382;
RA   Maeda Y., Moriguchi K., Kataoka M., Satou M., Satuti N., Tanaka N.,
RA   Yoshida K.;
RT   "Genome structure of Ri plasmid (1): Sequencing analysis of T-DNA and
RT   its flanking regions of pRi1724 in Japanese Agrobacterium
RT   rhizogenes.";
RL   Nucleic Acids Symp. Ser. 42:67-68(1999).
DR   EMBL; AP002086; BAB16216.1; -.
KW   Plasmid.
SQ   SEQUENCE   171 AA;  18295 MW;  730160B1FD0E0F52 CRC64;

  Query Match            72.9%;  Score 35;  DB 2;  Length 171;
  Best Local Similarity  71.4%;  Pred. No. 44;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 DAPIGYD 8
           | |:|||
Db      99 DGPVGYD 105


RESULT 6
Q9LZG9
ID   Q9LZG9      PRELIMINARY;      PRT;   180 AA.
AC   Q9LZG9;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   Hypothetical 19.8 kDa protein.
GN   T28A8_70.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Purnelle B., Boutry M., Goffeau A., Mewes H.W., Rudd S., Lemcke K.,
RA   Mayer K.F.X., Quetier F., Salanoubat M.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   EU Arabidopsis sequencing project;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL162691; CAB83150.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   180 AA;  19838 MW;  42A91B9998E18CFF CRC64;

  Query Match            72.9%;  Score 35;  DB 10;  Length 180;
  Best Local Similarity  75.0%;  Pred. No. 46;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 HDAPIGYD 8
           || ||| |
Db      38 HDIPIGVD 45


RESULT 7
Q9R6J9
ID   Q9R6J9      PRELIMINARY;      PRT;   199 AA.
AC   Q9R6J9;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   TIORF60 protein.
GN   TIORF60.
OS   Agrobacterium tumefaciens.
OG   Plasmid pTi-SAKURA.
OC   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC   Rhizobiaceae; Rhizobium.
OX   NCBI_TaxID=358;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MAFF301001;
RX   MEDLINE=20184752; PubMed=10721727;
RA   Suzuki K., Hattori Y., Uraji M., Ohta N., Iwata K., Murata K.,
RA   Katoh A., Yoshida K.;
RT   "Complete nucleotide sequence of a plant tumor-inducing Ti plasmid.";
RL   Gene 242:331-336(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MAFF301001;
RX   MEDLINE=98193120; PubMed=9524202;
RA   Suzuki K., Ohta N., Hattori Y., Uraji M., Katoh A., Yoshida K.;
RT   "Novel structural difference between nopaline- and octopine- type trbJ
RT   gene:construction of genetic and physical map and sequencing of
RT   trb/traI and rep gene clusters of a new Ti plasmid pTi-SAKURA.";
RL   Biochim. Biophys. Acta 1396:1-7(1998).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MAFF301001;
RA   Hattori Y., Suzuki K., Ohta N., Uraji M., Katoh A., Yoshida K.;
RT   "Genome structure of pTi-SAKURA(I): Strategy for DNA sequencing of a
RT   Japanese cherry-Ti plasmid.";
RL   Nucleic Acids Symp. Ser. 37:159-160(1998).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MAFF301001;
RA   Ohta N., Suzuki K., Hattori Y., Uraji M., Katoh A., Yoshida K.;
RT   "Genome structure of pTi-SAKURA (III): Characteristics of T-DNA.";
RL   Nucleic Acids Symp. Ser. 39:185-186(1998).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MAFF301001;
RA   Uraji M., Suzuki K., Ohta N., Hattori Y., Katoh A., Yoshida K.;
RT   "Genome structure of pTi-SAKURA (IV): Characteristics of tra region.";
RL   Nucleic Acids Symp. Ser. 39:187-188(1998).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MAFF301001;
RA   Hattori Y., Suzuki K., Ohta N., Uraji M., Katoh A., Yoshida K.;
RT   "Genome structure of pTi-SAKURA (V): Complete nucleotide sequence of
RT   plasmid pTi-SAKURA's vir region in Agrobacterium tumefaciens.";
RL   Nucleic Acids Symp. Ser. 39:265-266(1998).
DR   EMBL; AB016260; BAA87685.1; -.
KW   Plasmid.
SQ   SEQUENCE   199 AA;  21186 MW;  8488087E6D322126 CRC64;

  Query Match            72.9%;  Score 35;  DB 2;  Length 199;
  Best Local Similarity  71.4%;  Pred. No. 51;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 DAPIGYD 8
           | |:|||
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Db    127 DGPVGYD 133


RESULT 8
Q8U626
ID   Q8U626      PRELIMINARY;      PRT;   199 AA.
AC   Q8U626;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical protein Atu6109.
GN   ATU6109 OR AGR_PTI_204.
OS   Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OG   Plasmid pTiC58.
OC   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC   Rhizobiaceae; Rhizobium.
OX   NCBI_TaxID=176299;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21608550; PubMed=11743193;
RA   Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA   Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA   Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA   Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA   Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA   Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA   Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA   Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA   Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA   Nester E.W.;
RT   "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT   C58.";
RL   Science 294:2317-2323(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21608551; PubMed=11743194;
RA   Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA   Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA   Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA   Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA   Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
RA   Cielo C., Slater S.;
RT   "Genome sequence of the plant pathogen and biotechnology agent
RT   Agrobacterium tumefaciens C58.";
RL   Science 294:2323-2328(2001).
DR   EMBL; AE009430; AAL46345.1; -.
DR   EMBL; AE007938; AAK91070.1; -.
KW   Hypothetical protein; Plasmid; Complete proteome.
SQ   SEQUENCE   199 AA;  21117 MW;  DB7D89FF3478D04A CRC64;

  Query Match           72.9%;  Score 35;  DB 16;  Length 199;
  Best Local Similarity  71.4%;  Pred. No. 51;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 DAPIGYD 8
           | |:|||
Db     127 DGPVGYD 133


RESULT 9
Q8XHB1
ID   Q8XHB1      PRELIMINARY;      PRT;   218 AA.
AC   Q8XHB1;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Hypothetical protein CPE2574.
GN   CPE2574.
OS   Clostridium perfringens.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC   Clostridiales; Clostridiaceae; Clostridium.
OX   NCBI_TaxID=1502;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=13 / TYPE A;
RX   PubMed=11792842;
RA   Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA   Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT   "Complete genome sequence of Clostridium perfringens, an anaerobic
RT   flesh-eater.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR   EMBL; AP003194; BAB82280.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   218 AA;  25146 MW;  7B7AA90FBEB4DC3F CRC64;

  Query Match           72.9%;  Score 35;  DB 16;  Length 218;
  Best Local Similarity  71.4%;  Pred. No. 57;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 HDAPIGY 7
           | ||:||
Db     101 HSAPVGY 107


RESULT 10
Q9NAM5
ID   Q9NAM5      PRELIMINARY;      PRT;   371 AA.
AC   Q9NAM5;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Y105C5B.16 protein.
GN   Y105C5B.16.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   McMurray A.A.;
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99069613; PubMed=9851916;
RA   none;
RT   "Genome sequence of the nematode C.elegans: A platform for
RT   investigating biology.";
RL   Science 282:2012-2018(1998).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR   EMBL; AL110479; CAB54361.1; -.
DR   InterPro; IPR001175; Neur_channel.
DR   Pfam; PF02931; Neur_chan_LBD; 1.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW   Glycoprotein; Ionic channel; Postsynaptic membrane; Transmembrane.
SQ   SEQUENCE   371 AA;  43547 MW;  25A835F23D341D92 CRC64;

  Query Match           72.9%;  Score 35;  DB 5;  Length 371;
  Best Local Similarity  85.7%;  Pred. No. 1e+02;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 DAPIGYD 8
           | |||||
Db      59 DLPIGYD 65


RESULT 11
O74958
ID   O74958      PRELIMINARY;      PRT;   437 AA.
AC   O74958;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   Hypothetical serine-rich protein.
GN   SPCC736.12C.
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OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972H-;
RA   Wood V., Rajandream M.A., Barrell B.G., Murphy L., Harris D.;
RL   Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL023705; CAA19276.2; -.
SQ   SEQUENCE   437 AA;  48702 MW;  E0981EDE494A88A8 CRC64;

  Query Match             72.9%;  Score 35;  DB 3;  Length 437;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 HDAPIG 6
          ||||||
Db     76 HDAPIG 81


RESULT 12
Q9XSH5
ID   Q9XSH5      PRELIMINARY;      PRT;   457 AA.
AC   Q9XSH5;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   FK506-binding protein FKBP51.
OS   Saimiri boliviensis (Bolivian squirrel monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX   NCBI_TaxID=27679;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20539274; PubMed=11089542;
RA   Denny W.B., Valentine D.L., Reynolds P.D., Smith D.F., Scammell J.G.;
RT   "Squirrel Monkey Immunophilin FKBP51 Is a Potent Inhibitor of
RT   Glucocorticoid Receptor Binding.";
RL   Endocrinology 141:4107-4113(2000).
DR   EMBL; AF140759; AAD32678.1; -.
DR   HSSP; P27124; 1ROT.
DR   InterPro; IPR001179; FKBP_PPIase.
DR   InterPro; IPR001440; TPR.
DR   Pfam; PF00254; FKBP; 2.
DR   Pfam; PF00515; TPR; 2.
DR   PROSITE; PS00453; FKBP_PPIASE_1; 1.
DR   PROSITE; PS00454; FKBP_PPIASE_2; 1.
DR   PROSITE; PS50059; FKBP_PPIASE_3; 2.
SQ   SEQUENCE   457 AA;  51169 MW;  DFF9E1D81F7759A8 CRC64;

  Query Match             72.9%;  Score 35;  DB 6;  Length 457;
  Best Local Similarity   75.0%;  Pred. No. 1.3e+02;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 HDAPIGYD 8
          || |||  |
Db    196 HDIPIGID 203


RESULT 13
Q9XT11
ID   Q9XT11      PRELIMINARY;      PRT;   457 AA.
AC   Q9XT11;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   FK506-binding protein FKBP51.
GN   FKBP51.
OS   Aotus nancymaae (Owl monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX   NCBI_TaxID=37293;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Scammell J.G., Valentine D.L.;
RT   "Cloning and expression of owl monkey FKBP51 cDNA.";
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF141937; AAD33882.2; -.
DR   HSSP; P27124; 1ROT.
DR   InterPro; IPR001179; FKBP_PPIase.
DR   InterPro; IPR001440; TPR.
DR   Pfam; PF00254; FKBP; 2.
DR   Pfam; PF00515; TPR; 2.
DR   PROSITE; PS00453; FKBP_PPIASE_1; 1.
DR   PROSITE; PS00454; FKBP_PPIASE_2; 1.
DR   PROSITE; PS50059; FKBP_PPIASE_3; 2.
SQ   SEQUENCE   457 AA;  51297 MW;  56BB7EECEE290486 CRC64;

  Query Match             72.9%;  Score 35;  DB 6;  Length 457;
  Best Local Similarity   75.0%;  Pred. No. 1.3e+02;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 HDAPIGYD 8
          || |||  |
Db    196 HDIPIGID 203


RESULT 14
Q9XSI2
ID   Q9XSI2      PRELIMINARY;      PRT;   457 AA.
AC   Q9XSI2;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   FK506-binding protein FKBP51.
OS   Saguinus oedipus (Cotton-top tamarin).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
OX   NCBI_TaxID=9490;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Scammell J.G., Valentine D.L.;
RT   "Cloning and expression of cotton-top tamarin FKBP51 cDNA.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF143809; AAD33918.2; -.
DR   HSSP; P27124; 1ROT.
DR   InterPro; IPR001179; FKBP_PPIase.
DR   InterPro; IPR001440; TPR.
DR   Pfam; PF00254; FKBP; 2.
DR   Pfam; PF00515; TPR; 2.
DR   PROSITE; PS00453; FKBP_PPIASE_1; 1.
DR   PROSITE; PS00454; FKBP_PPIASE_2; 1.
DR   PROSITE; PS50059; FKBP_PPIASE_3; 2.
SQ   SEQUENCE   457 AA;  51116 MW;  F2D4E2A2B6658302 CRC64;

  Query Match             72.9%;  Score 35;  DB 6;  Length 457;
  Best Local Similarity   75.0%;  Pred. No. 1.3e+02;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 HDAPIGYD 8
          || |||  |
Db    196 HDIPIGID 203


RESULT 15
Q95L05
ID   Q95L05      PRELIMINARY;      PRT;   457 AA.
AC   Q95L05;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   FK506-binding protein FKBP51.
OS   Cercopithecus aethiops (Green monkey) (Grivet).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Cercopithecus.
OX   NCBI_TaxID=9534;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Denny W.B., Scammell J.G.;
RT   "African Green Monkey Immunophilin FKBP51.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY044168; AAK95405.1; -.
DR   InterPro; IPR001179; FKBP_PPIase.
DR   InterPro; IPR001440; TPR.
DR   Pfam; PF00254; FKBP; 2.
DR   Pfam; PF00515; TPR; 2.
DR   PROSITE; PS00454; FKBP_PPIASE_2; UNKNOWN_1.
DR   PROSITE; PS50059; FKBP_PPIASE_3; 2.
SQ   SEQUENCE   457 AA;  51095 MW;  9CB4CA338CF75144 CRC64;

  Query Match           72.9%;  Score 35;  DB 6;  Length 457;
  Best Local Similarity  75.0%;  Pred. No. 1.3e+02;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 HDAPIGYD 8
          || ||| |
Db    196 HDIPIGID 203


Search completed: March 14, 2003, 09:23:04
Job time : 32 secs
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FILE 'REGISTRY' ENTERED AT 12:42:49 ON 14 MAR 2003
L1 24 S HDAPIGYD/SQSP

FILE 'HCAPLUS' ENTERED AT 12:43:08 ON 14 MAR 2003
L2 16 S L1

L2 ANSWER 1 OF 16 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2003:129399 HCAPLUS
DOCUMENT NUMBER: 138:164734
TITLE: Animal model system for squamous cell carcinoma based on increased expression of recombinant protein kinase C.epsilon.
INVENTOR(S): Verma, Ajit K.; Reddig, Peter J.; Jansen, Aaron P.
PATENT ASSIGNEE(S): Wisconsin Alumni Research Foundation, USA
SOURCE: U.S., 16 pp.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 6521815	B1	20030218	US 2001-772647	20010130
US 2003051258	A1	20030313	US 2002-228931	20020827

PRIORITY APPLN. INFO.: US 2001-772647 A1 20010130

AB Non-human mammalian animals having a higher epidermal expression level of protein kinase C.epsilon. than their wild-type counterparts are phenotypically distinguished from wild-type animals in that the animals induced to develop tumors in a chem. initiation/promotion protocol are suppressed for subsequent papilloma development but are susceptible to developing squamous cell carcinoma and metastatic squamous cell carcinoma. The animals are advantageously used in methods for screening putative agents for altering the susceptibility, development and progression of squamous cell carcinoma and metastatic squamous cell carcinoma and have further com. value as tools for investigating the development of metastatic disease.

IT **497267-31-9**
RL: ADV (Adverse effect, including toxicity); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(amino acid sequence; animal model system for squamous cell carcinoma based on increased expression of recombinant protein kinase C.epsilon.)

REFERENCE COUNT: 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 2 OF 16 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2003:7668 HCAPLUS
DOCUMENT NUMBER: 138:164520
TITLE: Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
AUTHOR(S): Okazaki, Y.; Furuno, M.; Kasukawa, T.; Adachi, J.; Bono, H.; Kondo, S.; Nikaido, I.; Osato, N.;

Saito, R.; Suzuki, H.; Yamanaka, I.; Kiyosawa, H.; Yagi, K.; Tomaru, Y.; Hasegawa, Y.; Nogami, A.; Schoenbach, C.; Gojobori, T.; Baldarelli, R.; Hill, D. P.; Bult, C.; Hume, D. A.; Quackenbush, J.; Schriml, L. M.; Kanapin, A.; Matsuda, H.; Batalov, S.; Beisel, K. W.; Blake, J. A.; Bradt, D.; Brusic, V.; Chothia, C.; Corbani, L. E.; Cousins, S.; Dalla, E.; Dragani, T. A.; Fletcher, C. F.; Forrest, A.; Frazer, K. S.; Gaasterland, T.; Gariboldi, M.; Gissi, C.; Godzik, A.; Gough, J.; Grimmond, S.; Gustincich, S.; Hirokawa, N.; Jackson, I. J.; Jarvis, E. D.; Kanai, A.; Kawaji, H.; Kawasawa, Y.; Kedzierski, R. M.; King, B. L.; Konagaya, A.; Kurochkin, I. V.; Lee, Y.; Lenhard, B.; Lyons, P. A.; Maglott, D. R.; Maltais, L.; Marchionni, L.; McKenzie, L.; Miki, H.; Nagashima, T.; Numata, K.; Okido, T.; Pavan, W. J.; Pertea, G.; Pesole, G.; Petrovsky, N.; Pillai, R.; Pontius, J. U.; Qi, D.; Ramachandran, S.; Ravasi, T.; Reed, J. C.; Reed, D. J.; Reid, J.; Ring, B. Z.; Ringwald, M.; Sandelin, A.; Schneider, C.; Semple, C. A. M.; Setou, M.; Shimada, K.; Sultana, R.; Takenaka, Y.; Taylor, M. S.; Teasdale, R. D.; Tomita, M.; Verardo, R.; Wagner, L.; Wahlestedt, C.; Wang, Y.; Watanabe, Y.; Wells, C.; Wilming, L. G.; Wynshaw-Boris, A.; Yanagisawa, M.; Yang, I.; Yang, L.; Yuan, Z.; Zavolan, M.; Zhu, Y.; Zimmer, A.; Carninci, P.; Hayatsu, N.; Hirozane-Kishikawa, T.; Konno, H.; Nakamura, M.; Sakazume, N.; Sato, K.; Shiraki, T.; Waki, K.; Kawai, J.; Aizawa, K.; Arakawa, T.; Fukuda, S.; Hara, A.; Hashizume, W.; Imotani, K.; Ishii, Y.; Itoh, M.; Kagawa, I.; Miyazaki, A.; Sakai, K.; Sasaki, D.; Shibata, K.; Shinagawa, A.; Yasunishi, A.; Yoshino, M.; Waterston, R.; Lander, E. S.; Rogers, J.; Birney, E.; Hayashizaki, Y.

CORPORATE SOURCE: Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan

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DOCUMENT TYPE: Journal
LANGUAGE: English

AB Only a small proportion of the mouse genome is transcribed into mature mRNA transcripts. There is an international collaborative effort to identify all full-length mRNA transcripts from the mouse, and to ensure that each is represented in a phys. collection of clones. The manual annotation of 60,770 full-length mouse cDNA sequences is now reported. These are clustered into 33,409 'transcriptional units', contributing 90.1% of a newly established mouse transcriptome database. Of these transcriptional units, 4258 are new protein-coding and 11,665 are new non-coding messages, indicating that non-coding RNA is a major component of the

transcriptome. Forty-one percent of all transcriptional units showed evidence of alternative splicing. In protein-coding transcripts, 79% of splice variations altered the protein product. Whole-transcriptome analyses resulted in the identification of 2431 sense-antisense pairs. The present work, completely supported by phys. clones, provides the most comprehensive survey of a mammalian transcriptome so far, and is a valuable resource for functional genomics. The cDNA sequences are deposited in GenBank/EMBL/DDBJ under accession nos. AK002213-AK021412, AK027261-AK054560, AK075567-AK090394, and AK117103-AK117104. [This abstr. record is one of thirty records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT **493572-11-5**, GenBank BAC31430
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; anal. of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs)

L2 ANSWER 3 OF 16 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:869420 HCAPLUS
DOCUMENT NUMBER: 137:363111
TITLE: Psiepsilon RACK peptide composition and method for protection against tissue damage due to ischemia
INVENTOR(S): Mochly-Rosen, Daria
PATENT ASSIGNEE(S): USA
SOURCE: U.S. Pat. Appl. Publ., 17 pp.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2002168354	A1	20021114	US 2001-7363	20011109
PRIORITY APPLN. INFO.:			US 2000-247830P P	20001110

AB A method of reducing damage to cells and tissue caused by an ischemic or hypoxic event is disclosed. The method includes administering to the cell or tissue, either in vivo or ex vivo, .psi..epsilon.RACK peptide. The peptide can be administered before, during or after the ischemic or hypoxic event.

IT **207111-98-6**
RL: PAC (Pharmacological activity); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(.psi..epsilon.-RACK peptide compn. and method for protection against tissue damage due to ischemia)

L2 ANSWER 4 OF 16 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:777625 HCAPLUS
DOCUMENT NUMBER: 137:289003
TITLE: Pseudo-epsilon RACK (.psi..epsilon.RACK) peptide composition and method for protection against heart tissue damage due to ischemia
INVENTOR(S): Mochly-Rosen, Daria
PATENT ASSIGNEE(S): The Board of Trustees of the Leland Stanford Junior University, USA

SOURCE: PCT Int. Appl., 30 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002078600	A2	20021010	WO 2001-US51600	20011109

W: AU, CA, JP
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR

PRIORITY APPLN. INFO.: US 2000-274830P P 20001110

AB A method of reducing damage to cells and tissue in heart caused by an ischemic or hypoxic event is disclosed. The method includes administering to the cell or tissue, either in vivo or ex vivo, .psi..epsilon.RACK peptide. The peptide can be administered before, during or after the ischemic or hypoxic event.

IT **207111-98-6**
RL: PAC (Pharmacological activity); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(pseudo-epsilon RACK (.psi..epsilon.RACK) peptide compn. and method for protection against heart tissue damage due to ischemia)

L2 ANSWER 5 OF 16 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:616256 HCAPLUS
DOCUMENT NUMBER: 137:181594
TITLE: Dominant-negative variants of human protein kinases that inhibit the phosphorylation activity of their active enzyme isoforms
INVENTOR(S): Levine, Zurit; Bernstein, Jeanne
PATENT ASSIGNEE(S): Compugen Ltd., Israel
SOURCE: U.S. Pat. Appl. Publ., 170 pp., Cont.-in-part of U.S. Ser. No. 724,676.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2002110811	A1	20020815	US 2001-771161	20010126

PRIORITY APPLN. INFO.:
IL 2000-135619 A 20000512
IL 2000-136776 A 20000615
US 2000-724676 A2 20001128

AB The present invention concerns 91 nucleic acid sequences and amino acid sequences of variants of various human kinases, i.e. of sequences which inhibit activity of kinases in a dominant manner. The variants lack a domain or region required for phosphorylation, and thus may be dominant-neg. kinases obtained by alternative splicing of known original sequences of the kinase genes. The novel dominant-neg. kinase variants of the invention are not merely artificially truncated forms, fragments or mutations of known genes, but rather novel sequences which naturally occur within the body of individuals. The invention also concerns pharmaceutical compns. and

detection methods using these sequences.

IT **449216-82-4**
RL: ANT (Analyte); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(amino acid sequence; dominant-neg. variants of human protein kinases that inhibit the phosphorylation activity of their active enzyme isoforms)

IT **449225-92-7**
RL: PRP (Properties)
(unclaimed protein sequence; dominant-neg. variants of human protein kinases that inhibit the phosphorylation activity of their active enzyme isoforms)

L2 ANSWER 6 OF 16 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:539800 HCAPLUS
DOCUMENT NUMBER: 137:104169
TITLE: Use of an invertebrate system to identify modulators of the insulin signal transduction chain and the identification of effectors of insulin signal transduction
INVENTOR(S): Seidel-Dugan, Cynthia; Ferguson, Kimberly Carr; Kidd, Thomas
PATENT ASSIGNEE(S): Exelixis, Inc., USA
SOURCE: PCT Int. Appl., 232 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002055664	A2	20020718	WO 2002-US1048	20020111

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.:

US 2001-261226P	P	20010112
US 2001-261303P	P	20010112
US 2001-261304P	P	20010112
US 2001-261335P	P	20010112
US 2001-261336P	P	20010112
US 2001-261361P	P	20010112
US 2001-261456P	P	20010112
US 2001-261457P	P	20010112
US 2001-261458P	P	20010112
US 2001-261459P	P	20010112
US 2001-261461P	P	20010112
US 2001-261518P	P	20010112
US 2001-261531P	P	20010112
US 2001-261532P	P	20010112

US 2001-261589P P 20010112
US 2001-261590P P 20010112
US 2001-261694P P 20010112
US 2001-261695P P 20010112
US 2001-261697P P 20010112

AB A method of using invertebrate test systems to identify modulators of the insulin signal transduction pathway are described. These proteins are therapeutic targets for disorders assocd. with defective insulin receptor signaling. Methods for identifying modulators of ISM, comprising screening for agents that modulate the activity of ISM are provided. The genes for these regulators are then used to clone their human orthologs. Factors affecting the function of the Caenorhabditis elegans insulin receptor encoded by the daf-2 gene were screened for by their ability to revert a mutation leading to the dauer state. A Drosophila screen using a P-element carrying a GAL4-regulated promoter was used to identify external suppressors of a mutation in the Dinr gene. CDNA and protein sequences of human orthologs of these genes and proteins are presented.

IT **442703-09-5**
RL: PRP (Properties)
(unclaimed protein sequence; use of an invertebrate system to identify modulators of the insulin signal transduction chain and the identification of effectors of insulin signal transduction)

L2 ANSWER 7 OF 16 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:2517 HCAPLUS
DOCUMENT NUMBER: 137:237523
TITLE: Molecular transporters for peptides: delivery of a cardioprotective .epsilon.PKC agonist peptide into cells and intact ischemic heart using a transport system, R7
AUTHOR(S): Chen, Leon; Wright, Lee R.; Chen, Che-Hong; Oliver, Steven F.; Wender, Paul A.; Mochly-Rosen, Daria
CORPORATE SOURCE: Department of Molecular Pharmacology, Standford University School of Medicine, Standford, CA, 94305-5174, USA
SOURCE: Chemistry & Biology (2001), 8(12), 1123-1129
CODEN: CBOLE2; ISSN: 1074-5521
PUBLISHER: Elsevier Science Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Background: Recently, we reported a novel oligoguanidine transporter system, polyarginine (R7), which, when conjugated to spectroscopic probes (e.g., fluorescein) and drugs (e.g., cyclosporin A), results in highly water-sol. conjugates that rapidly enter cells and tissues. We report herein the prepn. of the first R7 peptide conjugates and a study of their cellular and organ uptake and functional activity. The octapeptide .psi..epsilon.RACK was selected for this study as it is known to exhibit selective .epsilon. protein kinase C isoenzyme agonist activity and to reduce ischemia-induced damage in cardiomyocytes. However, .psi..epsilon.RACK is not cell-permeable. Results: Here we show that an R7-.psi..epsilon.RACK conjugate readily enters cardiomyocytes, significantly outperforming .psi..epsilon.RACK conjugates of the transporters derived from HIV Tat and from Antennapedia. Moreover, R7-.psi..epsilon.RACK conjugate reduced

ischemic damage when delivered into intact hearts either prior to or after the ischemic insult. Conclusions: Our data suggest that R7 converts a peptide lead into a potential therapeutic agent for the ischemic heart.

IT **207111-98-6D**, conjugates **459146-74-8** **459146-76-0** **459146-77-1** **459146-78-2** **459146-82-8** **459146-86-2** **459146-88-4**
RL: PAC (Pharmacological activity); PKT (Pharmacokinetics); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(delivery of cardioprotective .epsilon.PKC agonist peptide into cells and intact ischemic heart using polyarginine transport system)

REFERENCE COUNT: 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 8 OF 16 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:763058 HCAPLUS
DOCUMENT NUMBER: 135:327323
TITLE: NMDA receptor complexes for diagnostic and therapeutic use
INVENTOR(S): Grant, Seth Garran Niels; Husi, Holger
PATENT ASSIGNEE(S): The University Court of the University of Edinburgh, UK
SOURCE: PCT Int. Appl., 202 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001077170	A2	20011018	WO 2001-GB1570	20010406
WO 2001077170	A3	20020328		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
EP 1272517	A2	20030108	EP 2001-917331	20010406
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				

PRIORITY APPLN. INFO.: GB 2000-8321 A 20000406
WO 2001-GB1570 W 20010406

AB The present invention provides multi-protein complexes, and sub-complexes thereof, and methods of producing the same. Preferably, the complexes comprise an NMDA receptor. The present invention further provides methods of identifying a compd. for treating disorders and conditions assocd. with dysfunction of NMDA receptors in the central nervous system. Addnl., there are provided methods of diagnosing or aiding diagnosis of disorders and

conditions assocd. with dysfunction of NMDA receptors in the central nervous system.

IT **148294-93-3 367633-06-5**, Protein (mouse clone P16054)
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(amino acid sequence; NMDA receptor complexes for diagnostic and therapeutic use)

L2 ANSWER 9 OF 16 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:910579 HCAPLUS
DOCUMENT NUMBER: 134:160633
TITLE: Evidence for functional role of .epsilon.PKC isozyme in the regulation of cardiac Ca2+ channels
AUTHOR(S): Hu, Keli; Mochly-Rosen, Daria; Boutjdir, Mohamed
CORPORATE SOURCE: Molecular and Cellular Cardiology Program, Veterans Affairs New York Harbor Healthcare System, Brooklyn, NY, 11209, USA
SOURCE: American Journal of Physiology (2000), 279(6, Pt. 2), H2658-H2664
CODEN: AJPHAP; ISSN: 0002-9513
PUBLISHER: American Physiological Society
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Limited information is available regarding the effects of protein kinase C (PKC) isoenzyme(s) in the regulation of L-type Ca2+ channels due to lack of isoenzyme-selective modulators. To dissect the role of individual PKC isoenzymes in the regulation of cardiac Ca2+ channels, we used the recently developed novel peptide activator of the .epsilon.PKC, .epsilon.V1-7, to assess the role of .epsilon.PKC in the modulation of L-type Ca2+ current (ICa,L). Whole cell ICa,L was recorded using patch-clamp technique from rat ventricular myocytes. Intracellular application of .epsilon.V1-7 (0.1 .mu.M) resulted in a significant inhibition of ICa,L by 27.9 .+-. 2.2% ($P < 0.01$, $n = 8$) in a voltage-independent manner. The inhibitory effect of .epsilon.V1-7 on ICa,L was completely prevented by the peptide inhibitor of .epsilon.PKC, .epsilon.V1-2 [5.2 .+-. 1.7%, not significant (NS), $n = 5$] but not by the peptide inhibitors of cPKC, .alpha.C2-4 (31.3 .+-. 2.9%, $P < 0.01$, $n = 6$) or .beta.C2-2 plus .beta.C2-4 (26.1 .+-. 2.9%, $P < 0.01$, $n = 5$). In addn., the use of a general inhibitor (GF-109203X, 10 .mu.M) of the catalytic activity of PKC also prevented the inhibitory effect of .epsilon.V1-7 on ICa,L (7.5 .+-. 2.1%, NS, $n = 6$). In conclusion, we show that selective activation of .epsilon.PKC inhibits the L-type Ca channel in the heart.

IT **207111-98-6**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(.epsilon.V1-7 peptide activator of .epsilon.PKC isoenzyme in regulation of cardiac Ca2+ channels)

REFERENCE COUNT: 43 THERE ARE 43 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 10 OF 16 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1999:728943 HCAPLUS
DOCUMENT NUMBER: 132:44701
TITLE: Sustained in vivo cardiac protection by a rationally designed peptide that causes .epsilon. protein kinase C translocation
AUTHOR(S): Dorn, Gerald W., II; Souroujon, Miriam C.; Liron, Tamar; Chen, Che-Hong; Gray, Mary O.; Zhou, Hui Zhong; Csukai, Michael; Wu, Guangyu; Lorenz, John N.; Mochly-Rosen, Daria
CORPORATE SOURCE: Department of Medicine, University of Cincinnati, Cincinnati, OH, 45167-0590, USA
SOURCE: Proceedings of the National Academy of Sciences of the United States of America (1999), 96(22), 12798-12803
CODEN: PNASA6; ISSN: 0027-8424
PUBLISHER: National Academy of Sciences
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Brief periods of cardiac ischemia trigger protection from subsequent prolonged ischemia (preconditioning). .epsilon. Protein kinase C (.epsilon.PKC) has been suggested to mediate preconditioning. Here, we describe an .epsilon.PKC-selective agonist octapeptide, .psi..epsilon. receptor for activated C-kinase (.psi..epsilon.RACK), derived from an .epsilon.PKC sequence homologous to its anchoring protein, .epsilon.RACK. Introduction of .psi..epsilon.RACK into isolated cardiomyocytes, or its postnatal expression as a transgene in mouse hearts, increased .epsilon.PKC translocation and caused cardioprotection from ischemia without any deleterious effects. Our data demonstrate that .epsilon.PKC activation is required for protection from ischemic insult and suggest that small mols. that mimic this .epsilon.PKC agonist octapeptide provide a powerful therapeutic approach to protect hearts at risk for ischemia.

IT **207111-98-6**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(sustained in vivo cardiac protection by a rationally designed peptide that causes .epsilon. protein kinase C translocation in transgenic mice)

REFERENCE COUNT: 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 11 OF 16 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1998:268373 HCAPLUS
DOCUMENT NUMBER: 128:317275
TITLE: Isoenzyme-specific peptide activators of protein kinase C, therapeutic methods to reduce ischemia injury, compositions, and screening methods
INVENTOR(S): Mochly-Rosen, Daria
PATENT ASSIGNEE(S): Board of Trustees of the Leland Stanford Junior University, USA
SOURCE: PCT Int. Appl., 47 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9817299	A1	19980430	WO 1997-US18716	19971017
W: CA, JP				
RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
US 6165977	A	20001226	US 1997-953033	19971017
PRIORITY APPLN. INFO.:			US 1996-28724P P	19961018

AB Isoenzyme-specific agonists or activators of .epsilon.PKC are disclosed. The agonists include peptides corresponding to the region of .epsilon.PKC between about amino acids 85 and 92. Also disclosed are therapeutic methods employing such .epsilon.PKC-specific agonists to induce preconditioning and thereby reduce injury due to subsequent ischemia, as well as methods for screening test compds. for .epsilon.PKC-selective agonist properties.

IT **207111-98-6**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(isoenzyme-specific peptide activators of protein kinase C, therapeutic methods to reduce ischemia injury, compns., and screening methods)

L2 ANSWER 12 OF 16 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1993:423577 HCAPLUS
DOCUMENT NUMBER: 119:23577
TITLE: Sequence and expression of human protein kinase C-.epsilon.
AUTHOR(S): Basta, Patricia; Strickland, Mary Beth; Holmes, William; Loomis, Carson R.; Ballas, Lawrence M.; Burns, David J.
CORPORATE SOURCE: Mol. Biol. Sect., Sphinx Pharm. Corp., Durham, NC, USA
SOURCE: Biochimica et Biophysica Acta (1992), 1132(2), 154-60
CODEN: BBACAQ; ISSN: 0006-3002
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Two human homologs of protein kinase C-.epsilon. (E1 and E2) were isolated from two distinct cDNA libraries. Sequence comparisons to PKC-.epsilon. cDNAs from several species indicated that each of these human .epsilon. clones contained cloning artifacts. Thus, a composite PKC-.epsilon. (E3) clone was derived from clones E1 and E2. Human PKC-.epsilon. (E3) has an overall sequence identity of 90-92% at the nucleotide level compared to the previously characterized mouse, rat and rabbit clones. At the amino acid level, the deduced human .epsilon. sequence shows a 98-99% identity with the mouse, rat and rabbit sequences. Expression of the human PKC-.epsilon. clone in S19 cells confirmed that the recombinant protein displayed protein kinase C activity and phorbol ester binding activity. The recombinant protein was also recognized by two distinct .epsilon.-specific polyclonal antibodies.

IT **148294-93-3**
RL: PRP (Properties); BIOL (Biological study)
(amino acid sequence of, complete)

L2 ANSWER 13 OF 16 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1990:453672 HCAPLUS
DOCUMENT NUMBER: 113:53672
TITLE: Cloning and expression and sequence of rat protein kinase C genes
INVENTOR(S): Ono, Katsutaka; Fujii, Tomoko; Igarashi, Koichi
PATENT ASSIGNEE(S): Takeda Chemical Industries, Ltd., Japan
SOURCE: Jpn. Kokai Tokkyo Koho, 23 pp.
CODEN: JKXXAF
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
JP 02000433	A2	19900105	JP 1988-249774	19881005
JP 2771188	B2	19980702		

PRIORITY APPLN. INFO.: JP 1987-252506 19871008
AB The cDNAs encoding the types .delta. and .epsilon. of protein kinase C of rat were cloned and expressed in Escherichia coli. The cloned genes were also transferred to yeast, Bacillus subtilis, and mammalian cell lines for expression. Nucleotide sequences of the cDNAs are given.
IT **116978-12-2**
RL: PRP (Properties)
(amino acid sequence of)

L2 ANSWER 14 OF 16 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1989:627755 HCAPLUS
DOCUMENT NUMBER: 111:227755
TITLE: Unique substrate specificity and regulatory properties of PKC-.epsilon.: a rationale for diversity
AUTHOR(S): Schaap, Dick; Parker, Peter J.; Bristol, Andrew; Kriz, Ron; Knopf, John
CORPORATE SOURCE: Ludwig Inst. Cancer Res., London, UK
SOURCE: FEBS Letters (1989), 243(2), 351-7
CODEN: FEBLAL; ISSN: 0014-5793
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Protein kinase C (PKC)-.epsilon. was isolated from a murine brain cDNA library. The clone, .lambda.61PKC-.epsilon., encoded a polypeptide of 737 amino acids that is homologous to other PKCs. Northern anal. showed that the 7 kb mRNA for this cDNA is widely expressed. The protein, when expressed in COS-1 cells, displayed phorbol ester-binding activity. However in order to detect the kinase activity of PKC-.epsilon., it was necessary to employ a synthetic peptide substrate based upon the pseudosubstrate site. Subsequent anal. demonstrated that PKC-.epsilon., while showing certain properties characteristic of the PKC family, has a quite distinct substrate specificity and is independent of Ca2+.
IT **123514-78-3**
RL: PRP (Properties); BIOL (Biological study)
(amino acid sequence of)

L2 ANSWER 15 OF 16 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1989:52097 HCAPLUS

DOCUMENT NUMBER: 110:52097
TITLE: A novel phorbol ester receptor/protein kinase, nPKC, distantly related to the protein kinase C family
AUTHOR(S): Ohno, Shigeo; Akita, Yoshiko; Konno, Yasuhiko; Imajoh, Shinobu; Suzuki, Koichi
CORPORATE SOURCE: Dep. Mol. Biol., Tokyo Metrop. Inst. Med. Sci., Tokyo, 113, Japan
SOURCE: Cell (Cambridge, MA, United States) (1988), 53(5), 731-41
CODEN: CELLB5; ISSN: 0092-8674
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Protein kinase C (PKC)-related cDNA clones encode an 84-kd protein, nPKC. Protein nPKC contains a cysteine-rich repeat sequence homologous to that seen in conventional PKCs (.alpha., .beta..lambda., .beta.II, and .gamma.), which make up a family of 77-78-kd proteins with closely related sequences. Protein nPKC, when expressed in COS cells, confers increased high-affinity phorbol ester receptor activity to intact cells. Antibodies raised against nPKC identified a 90-kd protein in rabbit brain ext. as well as in exts. from COS cells transfected with the cDNA construct. Protein nPKC shows protein kinase activity that is regulated by phospholipid, diacylglycerol, and phorbol ester but is independent of Ca2+. The structural and enzymol. characteristics of nPKC clearly distinguish it from conventional PKCs, which until now have been the only substances believed to mediate the various effects of diacylglycerol and phorbol esters. These results suggest an addnl. signaling pathway involving nPKC.

IT **116412-30-7**
RL: PRP (Properties)
(amino acid sequence of)

L2 ANSWER 16 OF 16 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1988:585985 HCAPLUS
DOCUMENT NUMBER: 109:185985
TITLE: The structure, expression, and properties of additional members of the protein kinase C family
AUTHOR(S): Ono, Yoshitaka; Fujii, Tomoko; Ogita, Koji; Kikkawa, Ushio; Igarashi, Koichi; Nishizuka, Yasutomi
CORPORATE SOURCE: Cent. Res. Div., Takeda Chem. Ind., Osaka, 532, Japan
SOURCE: Journal of Biological Chemistry (1988), 263(14), 6927-32
CODEN: JBCHA3; ISSN: 0021-9258
DOCUMENT TYPE: Journal
LANGUAGE: English

AB In rat brain, 3 members of the protein kinase C family encoded by cDNAs, termed .delta., .epsilon., and .zeta., were newly identified by mol. cloning and sequence anal. The new members exhibited a common structure that was closely related to but clearly distinct from the 4 members of the family previously isolated having .alpha.-, .beta.I-, .beta.II-, and .gamma.-sequences, although the .zeta.-cDNA available at present did not appear to contain a complete reading frame for protein kinase C. The protein kinase .delta.-, .epsilon.-, and .zeta.-cDNAs all encoded a characteristic

cysteine-rich sequence and protein kinase domain sequence, both of which were highly homologous among the protein kinase C family. However, the new members lacked one of the conserved regions that was present in the .alpha.-, .beta.I, .beta.II-, and .gamma.-sequences. An addnl. cDNA clone termed .epsilon.' was isolated, which was identical with .epsilon.-cDNA except for a short sequence at the 5'-terminal end region. The 2 members having .delta.- and .epsilon.-sequences were expressed in COS 7 cells, and partially purified and characterized. The enzymes having .delta.- and .epsilon.-sequences depended on phospholipid and diacylglycerol for the enzymic activity, but their properties differed slightly from the previously known members of protein kinase C. Northern blot anal. suggested that the new members of protein kinase C exist in the brain and some other tissues.

IT **116978-12-2**
RL: PRP (Properties); BIOL (Biological study)
(amino acid sequence of, gene-derived)

E1 THROUGH E18 ASSIGNED

FILE 'REGISTRY' ENTERED AT 12:43:34 ON 14 MAR 2003
L3 18 SEA FILE=REGISTRY ABB=ON PLU=ON (207111-98-6/BI OR 116978-12-2/BI OR 148294-93-3/BI OR 116412-30-7/BI OR 123514-78-3/BI OR 367633-06-5/BI OR 442703-09-5/BI OR 449216-82-4/BI OR 449225-92-7/BI OR 459146-74-8/BI OR 459146-76-0/BI OR 459146-77-1/BI OR 459146-78-2/BI OR 459146-82-8/BI OR 459146-86-2/BI OR 459146-88-4/BI OR 493572-11-5/BI OR 497267-31-9/BI)

L3 ANSWER 1 OF 18 REGISTRY COPYRIGHT 2003 ACS
RN **497267-31-9** REGISTRY
CN INDEX NAME NOT YET ASSIGNED
SQL 737
MF Unspecified
CI MAN

REFERENCE 1: 138:164734

L3 ANSWER 2 OF 18 REGISTRY COPYRIGHT 2003 ACS
RN **493572-11-5** REGISTRY
CN GenBank BAC31430 (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank BAC31430 (Translated from: GenBank AK042994)
SQL 125
MF Unspecified
CI MAN

REFERENCE 1: 138:164520

L3 ANSWER 3 OF 18 REGISTRY COPYRIGHT 2003 ACS
RN **459146-88-4** REGISTRY
CN L-Aspartic acid, L-cysteinyl-L-histidyl-L-.alpha.-aspartyl-L-alanyl-L-prolyl-L-isoleucylglycyl-L-tyrosyl-, (1.fwdarw.1')-disulfide with L-cysteinyl-D-arginyl-D-arginyl-D-arginyl-D-arginyl-D-arginyl-D-arginyl-D-argininamide (9CI) (CA INDEX NAME)
SQL 17,9,8
MF C87 H149 N41 O23 S2

REFERENCE 1: 137:237523

L3 ANSWER 4 OF 18 REGISTRY COPYRIGHT 2003 ACS
RN **459146-86-2** REGISTRY
CN L-Aspartic acid, L-cysteinyl-L-histidyl-L-.alpha.-aspartyl-L-alanyl-L-prolyl-L-isoleucylglycyl-L-tyrosyl-, (1.fwdarw.1')-disulfide with L-cysteinyl-L-arginyl-L-arginyl-L-arginyl-L-arginyl-L-arginyl-L-arginyl-L-argininamide (9CI) (CA INDEX NAME)
SQL 17,9,8
MF C87 H149 N41 O23 S2

REFERENCE 1: 137:237523

L3 ANSWER 5 OF 18 REGISTRY COPYRIGHT 2003 ACS
RN **459146-82-8** REGISTRY
CN L-Aspartic acid, L-arginyl-L-arginyl-L-arginyl-L-arginyl-L-arginyl-L-arginyl-L-arginyl-L-arginyl-6-aminohexanoyl-L-cysteinyl-L-histidyl-L-.alpha.-aspartyl-L-alanyl-L-prolyl-L-isoleucylglycyl-L-tyrosyl- (9CI) (CA INDEX NAME)
SQL 17
MF C90 H154 N40 O23 S

REFERENCE 1: 137:237523

L3 ANSWER 6 OF 18 REGISTRY COPYRIGHT 2003 ACS
RN **459146-78-2** REGISTRY
CN L-Aspartic acid, L-arginyl-L-arginyl-L-arginyl-L-arginyl-L-arginyl-L-arginyl-L-arginyl-L-arginyl-L-cysteinyl-L-histidyl-L-.alpha.-aspartyl-L-alanyl-L-prolyl-L-isoleucylglycyl-L-tyrosyl- (9CI) (CA INDEX NAME)
SQL 16
MF C84 H143 N39 O22 S

REFERENCE 1: 137:237523

L3 ANSWER 7 OF 18 REGISTRY COPYRIGHT 2003 ACS
RN **459146-77-1** REGISTRY
CN L-Aspartic acid, L-cysteinyl-L-histidyl-L-.alpha.-aspartyl-L-alanyl-L-prolyl-L-isoleucylglycyl-L-tyrosyl-, (1.fwdarw.1')-disulfide with L-cysteinyl-L-lysyl-L-lysyl-L-lysyl-L-lysyl-L-lysyl-L-lysyl-L-lysinamide (9CI) (CA INDEX NAME)
SQL 17,9,8
MF C87 H149 N27 O23 S2

REFERENCE 1: 137:237523

L3 ANSWER 8 OF 18 REGISTRY COPYRIGHT 2003 ACS
RN **459146-76-0** REGISTRY
CN L-Argininamide, L-cysteinyl-L-arginyl-L-lysyl-L-lysyl-L-arginyl-L-arginyl-L-glutaminyl-L-arginyl-L-arginyl-, (1.fwdarw.1')-disulfide with L-cysteinyl-L-histidyl-L-.alpha.-aspartyl-L-alanyl-L-prolyl-L-isoleucylglycyl-L-tyrosyl-L-aspartic acid (9CI) (CA INDEX NAME)
SQL 19,10,9
MF C98 H169 N43 O26 S2

REFERENCE 1: 137:237523

L3 ANSWER 9 OF 18 REGISTRY COPYRIGHT 2003 ACS
RN **459146-74-8** REGISTRY

CN L-Lysinamide, L-cysteinyl-L-arginyl-L-glutaminyl-L-isoleucyl-L-lysyl-L-isoleucyl-L-tryptophyl-L-phenylalanyl-L-glutaminyl-L-asparaginyl-L-arginyl-L-arginyl-L-methionyl-L-lysyl-L-tryptophyl-L-lysyl-, (1.fwdarw.1')-disulfide with L-cysteinyl-L-histidyl-L-.alpha.-aspartyl-L-alanyl-L-prolyl-L-isoleucylglycyl-L-tyrosyl-L-aspartic acid (9CI) (CA INDEX NAME)
SQL 26,17,9
MF C149 H231 N47 O35 S3

REFERENCE 1: 137:237523

L3 ANSWER 10 OF 18 REGISTRY COPYRIGHT 2003 ACS
RN **449225-92-7** REGISTRY
CN 195: PN: US20020110811 SEQID: 195 unclaimed protein (9CI) (CA INDEX NAME)
SQL 737
MF Unspecified
CI MAN

REFERENCE 1: 137:181594

L3 ANSWER 11 OF 18 REGISTRY COPYRIGHT 2003 ACS
RN **449216-82-4** REGISTRY
CN Kinase (phosphorylating), protein, C.epsilon. (human dominant-negative isoenzyme Nv-13) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 104: PN: US20020110811 SEQID: 104 claimed protein
SQL 156
MF Unspecified
CI MAN

REFERENCE 1: 137:181594

L3 ANSWER 12 OF 18 REGISTRY COPYRIGHT 2003 ACS
RN **442703-09-5** REGISTRY
CN 2: PN: WO02055664 SEQID: 2 unclaimed protein (9CI) (CA INDEX NAME)
SQL 737
MF Unspecified
CI MAN

REFERENCE 1: 137:104169

L3 ANSWER 13 OF 18 REGISTRY COPYRIGHT 2003 ACS
RN **367633-06-5** REGISTRY
CN Protein (mouse clone P16054) (9CI) (CA INDEX NAME)
SQL 737
MF Unspecified
CI MAN

REFERENCE 1: 135:327323

L3 ANSWER 14 OF 18 REGISTRY COPYRIGHT 2003 ACS
RN **207111-98-6** REGISTRY
CN L-Aspartic acid, L-histidyl-L-.alpha.-aspartyl-L-alanyl-L-prolyl-L-isoleucylglycyl-L-tyrosyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1: PN: US20020168354 SEQID: 2 claimed
CN 1: PN: WO02078600 SEQID: 2 claimed protein

SQL 8
MF C39 H54 N10 O14

REFERENCE 1: 137:363111

REFERENCE 2: 137:289003

REFERENCE 3: 137:237523

REFERENCE 4: 134:160633

REFERENCE 5: 132:44701

REFERENCE 6: 128:317275

L3 ANSWER 15 OF 18 REGISTRY COPYRIGHT 2003 ACS
RN **148294-93-3** REGISTRY
CN Kinase (phosphorylating), protein (human clone E3 C isoenzyme .epsilon. reduced) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN Protein (human clone Q02156)
CN Protein kinase C-.epsilon. (human clone E3 reduced)
SQL 737
MF Unspecified
CI MAN

REFERENCE 1: 135:327323

REFERENCE 2: 119:23577

L3 ANSWER 16 OF 18 REGISTRY COPYRIGHT 2003 ACS
RN **123514-78-3** REGISTRY
CN Kinase (phosphorylating), protein (mouse clone .lambda.61PKC-.epsilon. C isoenzyme .epsilon. reduced) (9CI) (CA INDEX NAME)
SQL 737
MF Unspecified
CI MAN

REFERENCE 1: 111:227755

L3 ANSWER 17 OF 18 REGISTRY COPYRIGHT 2003 ACS
RN **116978-12-2** REGISTRY
CN Kinase (phosphorylating), protein (rat brain clone .lambda.CKR.epsilon.41 C isoenzyme .epsilon. reduced) (9CI) (CA INDEX NAME)
SQL 737
MF Unspecified
CI MAN

REFERENCE 1: 113:53672

REFERENCE 2: 109:185985

L3 ANSWER 18 OF 18 REGISTRY COPYRIGHT 2003 ACS
RN **116412-30-7** REGISTRY
CN Kinase (phosphorylating), protein (rabbit clone RP38/R4 C protein moiety reduced) (9CI) (CA INDEX NAME)
SQL 736

MF Unspecified
CI MAN

REFERENCE 1: 110:52097

FILE 'HOME' ENTERED AT 12:44:03 ON 14 MAR 2003

Searcher : Shears 308-4994